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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AF128731 LOCUS Result No. REFERENCE TITLE JOURNAL Score uncultured soil bacterium C065 uncultured soil bacterium C065 Bacteria, environmental samples. 1 (bases 1 to 410) Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kuske, C. tevels of bacterial community diversity in four arid soil by cultivation and 16S rRNA gene cloning Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999) 410 bp DNA linear BCT 10-MAY-1999 Uncultured soil bacterium C065 16S ribosomal RNA, partial sequence. AF128731 AF128731.1 % Query Match 100 100 100 100 100 Length GI:4761945 В AY245486 AF469407 PFAMTSSU AF040972 AF040974 GS16SJ59 AY193246 AF469403 AF469398 AF128656 AF44231 AF280951 AF280951 AF193254 AF193029 AF193103 AF293558 AF242312 AF128705 AF442310 AF442310 AF342310 AF34 AY193166 AF172927 AY037620 AY193253 AF469392 AF432842 AF442309 AY242747 AY242748 AY037626 AY293557 AF040975 AY193167 AF128692 AF247784 AF040976 AF172926 AY245484 AF128731 ALIGNMENTS SUMMARIES AY245486 Unculture AF469407 Unculture M23443 p.falciparu AF040972 Hepatozoo AF040974 Plasmodiu X85243 Goordonia sp AF040968 Babesia b AF172925 Unculture AY037640 Unculture AY193243 Unculture AY037566 Unculture AY037566 Unculture AF442309 Tetrapisi AY242747 Unculture AY037626 Unculture AY037626 Unculture AY037620 Unculture AY037620 Unculture AY093553 Unculture AY093553 Unculture AY093640 Unculture AY193263 Unculture AY193246 Unculture AF469403 Unculture AF469407 Unculture AF469407 Unculture AF469407 Unculture AF469407 Unculture AF469407 Unculture AF128692 AF1247784 AF124656 AF442311 AF280951 AY193254 AY193029 AY193103 AY2935103 AY2935103 AY2935103 AY2935103 AF442310 AF128731 Unculture Description BCT 10-MAY-1999 soils compared Eimeria m Eimeria m Unculture Unculture Unculture Eimeria m Eimeria m Unculture Tetrapisi Unculture Unculture Tetrapisi Unculture Unculture Unculture Tetrapisi Unculture Unculture

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2 (bases 1 to 420)
Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kuske, C.R.
Direct Submitssion
Submitted (15-FEB-1999) Environmental Molecular Biology, Life
Submitted (15-FEB-1999) Mational Laboratory, M888, Los
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Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kuske, C.
Direct Submission
Submitted (15-FEB-1999) Environmental Molecular Biology,
Sciences Division, Los Alamos National Laboratory, M888,
Alamos, NM 87545, USA
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Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kuske, C.R.
Levels of bacterial community diversity in four arid soils compared
by cultivation and 16S rRNA gene cloning
Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
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/product="16S ribosomal RNA"
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/mol_type="genomic DNA"
/db_xref="taxon:92314"
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/mol_type="genomic DNA"
/db_xref="taxon:92353"
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Direct Submission
Submitted (08-SEP-2000) Faculty of Agricultural and
Submitted (08-SEP-2000) Faculty of Agricultural and
Riological Sciences, Gent University, Coupure Links
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Submitted (23-MAR-2000) Faculty of Agricultural and minorical Sciences, Gent University, Coupure Links
2 (bases 1 to 440)
Dunbar, J., Takala, S.,
Direct Submission
Submitted (15-FEB-199)
                                                                                                                                                                               uncultured soil bacterium CO108
uncultured soil bacterium CO108
Bacteria; environmental samples.
1 (bases 1 to 440)
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On Sep 8, 2000 this sequence version replaced gi:9864056
Location/Qualifiers
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Dejonghe, W.L., Goris, J., E
Verstraete, W. and Top, E.M.
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Dejonghe, W.L., Goris, J., E
Verstraete, W. and Top, E.M.
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                                                                                                         Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. Levels of bacterial community diversity in f by cultivation and 16s rRNA gene cloning Appl. Environ. Microbiol. 65 (4), 1662-1669
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/mol type="genomic DNA"
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/noTe="isolated from B-horizon
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sequence.
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                          AF280951 50
Uncultured bacterium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kurtzman,C.P. and Robnett,C.J.

Phylogenetic relationships among yeasts of the 'Saccharomyces complex' determined from multigene sequence analyses

FEMS Yeast Res. 3 (4), 417-432 (2003)
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Tetrapisispora arboricola small subunit ribosomal RNA gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 495)
Kurtzman, C.P. and Robnett, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Tetrapisispora.
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/mol_type="genomic DNA"
/db_xref="taxon:92278"
/clone="C0108"
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/clone="A314"
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/strain="NRRL Y-27308"
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                                                                                                                                                                   Unpublished (bases 1 to 508)
2 (bases 1 to 508)
2 Harris, J.Kirk., Kelley, S.T. and Pace, N.R.
Harris, J.Kirk., Kelley, S.T. and Pace, N.R.
Direct Submission
Submitted (10-DEC-2002) Molecular, Cellular and Developmental
Submitted (10-DEC-2002) Molecular, Cellular and Developmental
Submitted (10-DEC-2002) Molecular, Cellular and Developmental
Submitted (10-DEC-2002) Molecular, Cempus box 347, Boulder, CO 80309,
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3 (bases 1 to 500)
Stach, J.E., Bathe, S. and Burns, R.G.
Strect Submission
Submitted (20-JUN-2000) Biosciences, University
Submitted (20-JUN-2000) Rosciences, University
Submitted (20-JUN-2000) Rosciences, University
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1 (bases 1 to 500)

Stach, J.E., Bathe, S., Clapp, J.P. and Burns, R.G.

PCR-SSCP comparison of 16S rDNA sequence diversity in soil DNA obtained using different isolation and purification methods FEMS Microbiol. Ecol. 36 (2-3), 139-151 (2001)
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New perspective on uncultured bacterial phylogenetic
onpublished
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/mol_type="genomic DNA"
/db_xref="taxon:77133"
                 /product="16S ribosomal RNA"
                                                                                 /mol type="genomic DNA"
/isolation_source="marine
/db_xref="taxon:77133"
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Harris, J.Kirk., Kelley, S. 1. ..... - ... Direct Submission
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Direct Submission
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New perspective on uncultured bacterial phylogenetic division
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uncultured candidate division OP11,
Bacteria, candidate division OP11,
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Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
New perspective on uncultured bacterial ;
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                                                                                                                                  (bases 1 to 525)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="uncultured candidate division OP11
/mol type="genomic DNA"
/isoTation_source="contaminated aquifer"
/db xref="taxon:174293"
/clone="WSA86"
                                                                                                                                                                                                                                                                environmental samples.
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bacterium clone DA43
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RNA gene, partial sequence.
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ribosomal RNA
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RESULT' 11
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Best Local S
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JOURNAL
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AF442312 534 bp DNA linear PLN 11-JUN-2003
Tetrapisispora iriomotensis small subunit ribosomal RNA gene,
partial sequence; mitochondrial gene for mitochondrial product.
AF442312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uncultured phototrophic eukaryote clone gene, partial sequence; chloroplast gene AY293558
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-MAY-2003) Geology, University of Illinois,
Natural History Building, 1301 West Green St, Urbana, IL
Location/Qualifiers
                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonheyo, G.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 529)
Bonheyo, G.T., Fouke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chloroplast uncultured phototrophic eukaryote uncultured phototrophic eukaryote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frias-Lopez,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Partitioning of Mineralogical, Geochemical, and Microbial in Travertine Terraces at Yellowstone Hot Springs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dukaryota;
                                                                                                                                                                                                Similarity
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ilarity 100.0%;
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/mol_type="genomic_DNA"
/isolation_source="contaminated aquifer"
/db_xref="taxon:77133"
                                                                                                                                                                                                                                                           /product="16S ribosomal
                                                                                                                                                                                                                                                                                                     /db_xref="taxon:172788"
/clone="FL14G11"
                                                                                                                                                                                                                                                                                                                                                                               /organism="uncultured phototrophic
/organelle="plastid:chloroplast"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           environmental samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fouke, B.W., Martin, H.G., Veysey, J.,
                                                                                                                                                                                                                                                                                                                                                                    type="genomic DNA"
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                                                                                                                                                                                Score 21; DB 3;
Pred. No. 3.5e+02;
; Mismatches 0;
                                                                                                                         488
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FL14G11 16S ribosomal RNA
e for chloroplast product.
                                                                                                                                                                                                               Length 529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 GTGCCAGCAGCAGCGGTAATA 174
                                                                                                                                                                                                                                                                  Bacteria, Company Davis, J.A. and Kusk Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kusk Levels of bacterial community diversity in four arid by cultivation and 16S rRNA gene cloning by cultivation and 16S rRNA (199) and Environ. Microbiol. 65 (4), 1662-1669 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
AF128705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-NOV-2001) United States Department of Agriculture, National Center for Agricultural Utilization Research, 1815 N. University St., Peoria, IL 61604, USA
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Phylogenetic relationships among yeasts of the 'Saccharomyces complex' determined from multigene sequence analyses

FEMS Yeast Res. 3 (4), 417-432 (2003)
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccha
Saccharomycetales; Saccharomycetaceae; Tetrapisispora.
                                                                                                                                                    Sciences Division, Los Alamos National Alamos, NM 87545, USA
                                                                                                                                                                                                   2 (bases 1 to 550)
Dunbar, J., Takala, S., Barns, S.M., Davis, J.A.
Direct Submission
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                                                                                                                                                                                     Submitted (15-FEB-1999) Environmental
                                                                                                                                                                                                                                                                                                                                                                                              uncultured soil bacterium S0212 uncultured soil bacterium S0212
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Similarity 100.0%;
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/organelle="mitochondrion"
/mol_type="genomic_DNA"
/strain="NRRL Y-27309"
                                             /organism="uncultured so
/mol_type="genomic DNA"
/db_xref="taxon:92327"
/clone="50212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="small subunit ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:113606"
/clone="A315"
              /product="168 ribosomal
                                                                                                                                 ocation/Qualifiers
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n 80212 16S
                                                                                                  soil bacterium S0212
                  RNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribosomal RNA,
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l Laboratory, M888,
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                                                                                                                                                                                                                       and Kuske, C.R.
                                                                                                                                                                                                                                                                                                                                             and Kuske, C
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partial
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AY037640
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Best Local S
Matches 21
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                                                                                                                                                                                                                                                                                                                  177
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Submitted (02-NOV-2001) United States Department of Agriculture, National Center for Agricultural Utilization Research, 1815 N. University St., Peoria, IL 61604, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetrapisispora nanseiensis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Tetrapisispora.
Furlong, M.A., Singleton, D.R., Coleman, D.C. and Whitman, W. Molecular and culture-based analyses of prokaryotic commun from an agricultural soil and the burrows and casts of the earthworm Lumbricus rubellus
                                                                     Bacteria; environmental samples.
1 (bases 1 to 559)
                                                                                                        uncultured soil bacterium uncultured soil bacterium
                                                                                                                                                                                                          AY037640 559 bp Uncultured soil bacterium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phylogenetic relationships among yeasts of the 'Saccharomyces complex' determined from multigene sequence analyses FEMS Yeast Res. 3 (4), 417-432 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF442310 552 bp DNA linear PLN 11-c
Tetrapisispora nanseiensis small subunit ribosomal RNA gene
                                                                                                                                                            AY037640.1 GI:15789072
                                                                                                                                                                              partial sequence.
AY037640
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Kurtzman, C.P. and Robnett, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitochondrion Tetrapisispora nanseiensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="NRRL Y-27310"
/db_xref="taxon:113607"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="small subunit ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Tetrapisispora nanseiensis"
organelle="mitochondrion"
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Pred. No. 3.4e+02;
; Mismatches 0;
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Pred. No. 3.4e+02;
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S133 16S ribosomal RNA gene,
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                      communities of the
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AY193243
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VERSION
KEYWORDS
Search completed: August 4, 2004, 07:44:21 Job time : 921.446 secs
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                                                                                                                                             444 GTGCCAGCAGCAGCGGTAATA 464
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2 (bases I to 564)
2 (bases I to 564)
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11872477
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1 (bases 1 to 564)

Harris,J.Kirk., Kelley,S.T. and Pace,N.R.

New perspective on uncultured bacterial phylogenetic division OP11

Unpublished

Unpublished
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Oncultured bacterium clone Bol43 16S ribosomal RNA gene, partial
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Singleton,D.R., Furlong,M.A., Coleman,D.C. and Whitman,W.B.
Direct Submission
Submitted (31-MAY-2001) Department of Microbiology, University of
Georgia, 541 Biological Sciences Bldg, Athens, GA 30602-2605, USA
Location/Qualifiers
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AY193243
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/mol_type="genomic DNA"
/db_xref="taxon:164851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="uncultured bacterium"
'mol type="genomic DNA,"
'isolation, source="marine sediment"
'db_xref="taxon:77133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="Bol43"
environmental_sample
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100.0%; Pred. No. 3.4e+02;
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is the number of results predicted by chance to have a ater than or equal to the score of the result being printed,
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Sequence 9, Appli
Sequence 3170, Ap
Sequence 3171, Ap
Sequence 3171, Ap
Sequence 3, Appli
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Sequence 755, App
Sequence 728, Appli
Sequence 728, Appli
Sequence 476, Appli
Sequence 450, Appli
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Matches 20
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Patent No. 6054278
Patent No. 6054278
GENERAL INFORMATION:
APPLICANT: DODGE, Deborah E
APPLICANT: SWITH, DOUG
TITLE OF INVENTION: INDESONAL RNA GENE POLYMORPHISM BASED MICROORGANISM
TITLE OF INVENTION: INDESONAL RNA GENE POLYMORPHISM BASED MICROORGANISM
TITLE OF INVENTION: IDENTIFICATION
FILE REFERENCE: 4943 US
CURRENT APPLICATION NUMBER: US/09/073,465
CURRENT FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 17
SOOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 24
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                    APPLICANT: Hoshina, Sadayori
APPLICANT: Weinstein, I. Berna
TITLE OF INVENTION: Microorgan
TITLE OF INVENTION: Microorgan
TITLE OF INVENTION: Oligomers
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: COOPER & DUNHAM
ATTERETS: COOPER & DUNHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Unknown Organism: Bacterial
             ZIP: 10112
COMPUTER READABLE FORM:
                                                                                                                              STREET: 30 Rocke
CITY: New York
STATE: New York
                                                                                     COUNTRY:
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                                                                                                                                                                                                                             30 Rockefeller Plaza
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Conservative C
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DNA Oligomers For Use In Detection Of
Microorganisms And Methods Of Using St

Oligomers

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US-09-375-932A-5
US-09-317-099-5
US-09-13-377B-2
US-09-13-377B-2
US-09-191-099-6
US-09-191-099-6
US-09-191-099-6
US-09-191-099-2
US-09-191-099-2
US-09-191-099-2
US-09-191-099-2
US-09-193-377B-4
US-09-193-377B-4
US-09-193-377B-7
US-08-25-377B-7
US-08-25-377B-7
US-09-193-377B-8
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Pred. No. 0.016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    And Methods Of Using Such
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Result

Query Match

Length

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SUMMARIES

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US-09-107-532A-3171
US-08-979-86-3
US-09-577-640-3
US-09-328-111-75
US-08-953-171-72
US-08-953-171-72
US-09-328-111-476
US-09-328-111-476
US-09-328-111-476
US-09-328-111-476
US-07-898-905-1
US-07-898-905-2
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US-07-898-905-3
US-09-006-089-1
US-07-898-905-3
US-09-006-089-1

Minimum DB seq length: 0
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parameters:

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Scoring table: Sequence:

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Perfect score:

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GENERAL INFORMATION:
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Best Local
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PRIOR APPLICATION DATA:
PROPRICATION NUMBER: US 07/672
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3454
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                            APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
COMPUTER: II
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                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                            NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 100 Beaver Street
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212) 422523 COOP UI
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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NAME/KEY: misc feature; LOCATION: (B) LOCATION 1...279; SEQUENCE DESCRIPTION: SEQ ID NO: 3170: US-09-107-532A-3170
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US-09-107-532A-3171/c
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lyrn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
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Best Local Similarity
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TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3170:
SEQUENCE CHARACTERISTICS:
                                                                                                                TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3171:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 GCAAACAGGATTAGATACCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998
                                                         LENGTH: 279 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Waltham
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100.0%; Pred. No.
170.0%; Mismatches
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Pred. No. 0.014;
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...279;
SEQUENCE DESCRIPTION: SEQ ID NO: 3171;
US-09-107-532A-3171
                                           RESULT 6
US-09-577-640-3
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                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-08-979-586-3
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Patent No. 6190903
GENERAL INFORMATION:
APPLICANT: Weinstein, I. B., et
             Sequence 3, Application Patent No. 6420165
                                                                                                                                                                            Matches
                                                                                                                                                                                           Query Match
Best Local (
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                       TOPOLOGY: 111
MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNUBER: 28,678
REFERENCE/DOCKET NUMBER: 52208/JPW/JKM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100
STREET: New York
STATE: New York
STATE: U.S.A.
                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 538 base pairs
TYPE: nucleic acid
STRANDENESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Weinstein, TITLE OF INVENTION: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                            234 GCAAACAGGATTAGATACCC 253
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                                                                                                                                                                                             Similarity
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                                                                                                                                                                      100.0%; Score 20; DB 3; ilarity 100.0%; Pred. No. 0.013; Conservative 0; Mismatches
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M CAPABLE OF BIODEGRADATION OF
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CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 755
LENGTH: 571
TYPE: DNA
ORGANISM: Homo sapiens
  밁
                                                                                                                                              ; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(571)

; OTHER INFORMATION: n = A,T,C

US-09-328-111-755
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; ORGANISM: Bacillus midousuji
US-09-577-640-3
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CURRENT FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 08/979,586
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 3
LENGTH: 538
                                                                          Matches
                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Steinmann, Kathleen E. APPLICANT: Astle, Jon H. APPLICANT: Burgess, Christopher C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Burgess, Christopher C. APPLICANT: Bushnell, Steven E. APPLICANT: Carroll III, Eddie APPLICANT: Catino, Theodore J. Applicant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: The Trustees of Columbia University in the City of TITLE OF INVENTION: Bacterium Capable of Biodegradation of Wastes FILE REFERENCE: 52208apct
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REPERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Endege, Wilson O.
                                                                                        Local
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les 20; Conserv
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295
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                        GCAAACAGGATTAGATACCC 20
GCAAACAGGATTAGATACCC 314
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                                                                      100.0%; Silarity 100.0%; FConservative 0;
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Pred. No. 0.0
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RESULT 8 US-08-953-171-2 ; Sequence 2, Application US/08953171 ; Patent No. 6124094

ENERAL INFORMATION:

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APPLICANT: Endege, Wilson O.
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Best Local S
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APPLICANT:
                                                                                                                                                                                                                                       Patent No.
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                                                                                                                                                                           APPLICANT:
                                                                                     PPLICANT:
ILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Spratt, Gwendolyn DD
REGISTION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404 688 0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 17-OCT-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ZOOGLOBAL AND HYPHOTITLE OF INVENTION: SPP. NUCLEIC ACIDS NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
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              숙숙
                                                                                                                                                                                                                                                                                                                              241 GCAAACAGGATTAGATACCC 260
                                                                                                                                                                                                                                    728, Application US/09328111
5. 6262333
           T: Lewis, Marcia E.
T: Monahan, John E.
T: Schlegel, Robert
INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
INVENTION: PRODUCTS
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DEDNESS: single
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                                                                                                             Burgess, Christopher C. Bushnell, Steven E. Carroll III, Eddie Catino, Theodore J.
                                                                               Porti, Adman M.
                                                                                                                                                                         Steinmann, Kathleen E. Astle, Jon H.
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SAYLER, GARY
STAPLETON, RAYMOND
TOTAL AND HYPHOMICROBIUM
TOTAL ACIDS
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ilarity 100.0%;
Conservative 0
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LAYTON, ALICE
KELLY, CHIRSTINE
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Pred. No. 0.013;
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                                                                                             US-08-114-695A-5
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CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION UNDEER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FBSESEQ for Windows Version 3.0
SEQ ID NO 728
Query Match
Best Local Similarity 85.0
"Arches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08114695A Patent No. 5508193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local S
                                                                                                                                                                                                                      TELEPHONE: 612-339-033
TELEPAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)...(624)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (1)...(624)
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                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mandelbaum, Raphaeel APPLICANT: Wackett, Lawrence P TITLE OF INVENTION: DEGRADATION TITLE OF INVENTION: WATER NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: MUETING, ANN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 55402
                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SCHWEGMAN, L
STREET: 3500 IDS CENTER
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                                                                                                                                                                                                                            660 base pairs
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                                                                                                                Pseudomonas citronellolis
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100.0%; Pred. No. 0.013;
ative 0; Mismatches
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DEGRADATION OF S-TRIAZINES IN SOIL AND
                       100.0%; Score 20; DB 1; Length 660; 85.0%; Pred. No. 0.013; tive 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                           Query Match 100.0%; Score 20; DB 3; Length 672; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/07898905
Patent No. 5424187
GENERAL INFORMATION:
APPLICANT: SHORTKN:
TITLE OF INVENTION: "DIAGNOSIS AND TREATMENT OF ARTERIAL
TITLE OF INVENTION: CHLAMYDIAL GRANULOWA"
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct) TELEFAX: 1-206-224-0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIF: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ 1D NOS: 850
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ 1D NO 450
LENGTH: 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCETALING SISTEM, MS. CONTROLL SCENARE: Word for Windows-t CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/07/898,9
FILING DATE: 19920612
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: none
FILING DATE: none
ATTORNEY/AGENT INFORMATION:
NAME: Sundsmo, John, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET: NUMBER: UOFW-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 GCAAACAGGATTAGATACCC 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-328-111-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-07-898-905-1
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                                                                                                                                                                                                                                                                                                     Matches
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APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Burges, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll Manan
APPLICANT: Carlo, Theodore J.
APPLICANT: Carlo, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION WIMBER: US 60/088, 801
EARLIER APPLICATION NUMBER: US 60/088, 801
EARLIER APPLICATION NUMBER: US 60/088, 801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOSTWARE: PASTSEQ for Windows Version 3.0
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100.0%; Score 20; DB 3; Length 665;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 20; Conservative 0; Mismatches 0; Indels
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Sequence 450. Application US/09328111
Setent No. 626233
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Stelman, Kathleen E.
APPLICANT: Burges, Christopher C.
APPLICANT: Carroll III, Eddie
APPLICANT: Sord, Donna M.
APPLICANT: Marcia E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN
TITLE OF INVENTION: NOVEL HUMAN
TITLE OF INVENTION: NOVEL HUMAN
TITLE OF INVENTION: NOWBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
                                                                                                                                                                                        Sequence 476, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 GCAAACAGGATTAGATACCC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // LOCATION: (1)...(665)
// OTHER INFORMATION: n = A,T,C or G
US-09-328-111-476
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                                     50 GCAAACAGGAUUAGAUACCC 69
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                          RESULT 11
US-09-328-111-476
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US-09-328-111-450
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LENGTH: 665
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                 US-07-698-905-2
; Sequence 2, Application US/07898905
; Patent No. 5424187
; GENERAL INFORMATION:
    APPLICANT: Shor; Kuo
; TITLE OF INVENTION:
    TITLE OF INVENTION:
    NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
    STREET: 2800 Pacific First Center, 1420 Fifth Avenue
    CITY: Seattle
    STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 20; DB 1; Length 851; Best Local Similarity 100.0%; Pred. No. 0.012; Matches 20; Conservative 0; Mismatches 0; Indels
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Sequence 3, Application US/07898905
Batent NO. 5424187
GENERAL INTERMATION:
APPLICANT: Shor;Kuo
TITLE OF INVENTION: "DIAGNOSIS AND TREATMENT OF ARTERIAL
TITLE OF INVENTION: "CHLAMYDIAL GRANULOMA"
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READALE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM:
MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/898,905
FILING DATE: 19920612
FILING DATE: 19920612
FILING DATE: 19920612
FILING DATE: NOMER: NOME
FILING DATE: NOMER: NOME
FILING DATE: NOME
APPLICATION NUMBER: 34,446
REGISTRATION SEQ 100: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 851 base pairs
TYPE: MUCHEC CARACTERISTICS:
REGISTRATION POR SEQ 100: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 851 base pairs
TYPE: MUCHEC CARACTERISTICS:
REGISTRATION POR SEQ 100: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 851 base pairs
TYPE: MUCHEC CARACTERISTICS:
REGISTRATION POR SEQ 100: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 851 base pairs
TYPE: MUCHEC CARACTERISTICS:
REGISTRATION POR SEQ 100: 2:
SEQUENCE CHARACTERISTICS:
SEQ
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
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MOLECULE TYPE: genomic DNA
DESCRIPTION: Cpn
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ZIP: 98101-2347
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US-07-898-905-3
RESULT 14
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COMPUTER: IEM PC/386 Compatible
SOFTRARE: Word for Windows-t
CURRENT APPLICATION DATA:

PELLOATION NUMBER: US/07/898,905
FILING DATE: 19920612
CLASSIFICATION: 435
FILING DATE: OF WINDOWSER: OF WINDOWSER: OF FILING DATE: OF SECURITY OF
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Query Match
100.0%; Score 22; DB 2;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 22; Conservative 0; Mismatches 0
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MOLECULE TYPE: DNA (genomic)

US-07-923-871C-36
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Sequence 35, Appl
                                                                                                                  4, 2004, 06:01:54 ; Search time 39.759 Seconds (without alignments) 307.073 Million cell updates/sec
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(Ggn2 6/ptodata/2/ina/5A COMB.seq:*
(Ggn2 6/ptodata/2/ina/6B_COMB.seq:*
(Ggn2 6/ptodata/2/ina/6A_COMB.seq:*
(Ggn2 6/ptodata/2/ina/6B_COMB.seq:*
(Ggn2 6/ptodata/2/ina/PGTUS COMB.seq:*
(Ggn2 6/ptodata/2/ina/PGTUS COMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-09-052-333A-27

US-09-052-333A-29

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US-09-052-333A-29

US-09-052-333A-29

US-08-632-470-40

US-08-632-470-25

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Maximum DB seq length: 200000000
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Sequence 1, Ag
Sequence 48, P
Sequence 49, P
   Sequence 43,
Sequence 38,
Sequence 38,
Sequence 45,
Sequence 53,
Sequence 45,
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Sequence 1, A
Sequence 1, A
Sequence 2, A
Sequence 1, A
Sequence 1, A
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Patent No. 5912117
GENERAL INFORMATION:
APPLICANT: White Ph.D, Thomas J.
APPLICANT: Dodge, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Addresses: Addresses: Addresses: Addresses: Addresses: Addresses: Addresses: Addresses: Addresses: Nutley
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,871C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 0-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: PETEY, DOUGHAS A.
REGISTRATION NUMBER: 8697
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (510) 814-2977
2 US-08-632-470-43
2 US-08-632-470-46
2 US-08-632-470-38
2 US-08-632-470-38
2 US-08-632-470-45
2 US-08-632-470-44
4 US-09-198-452A-1
1 US-08-943-464-1
1 US-08-943-464-1
1 US-08-941-384-1
4 US-09-491-384-1
4 US-09-491-384-1
4 US-09-61-770-1
2 US-08-633-470-48
2 US-08-633-470-48
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COUNTY: USA
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DO
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US-07-923-871C-35/C
US-07-923-871C-35/C
US-07-923-871C-35/C
US-07-923-871C-35/C
US-07-923-871C-35/C
US-07-923-871C-31-37

GENERAL INFORMATION:
HATCH BY BADDICANT: White Ph.D, Thomas J.
APPLICANT: White Ph.D, Thomas J.
APPLICANT: Dodge, Deborah E.
ITILE OF INVENTION: 38

CORRESPONDENCE ADDRESS:
ADDRESSE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STARE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
COUNTRY: USA
COUNTRE READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.25
COMPUTER: BAP PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/923,871C
FILING DATE: 07-MAR-1990
ATTORNEY/AGRATION:
APPLICATION NUMBER: 35,321
RESERRENCE/OCCET NUMBER: 35,321
RESERRENCE/OCCET NUMBER: 8697
TELEPHONE: (510) 814-2977
TELEPHONE: (510) 814-2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 22; DB 2; Length 370; 100.0%; Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: White Ph.D, Thomas J.
APPLICANT: White Ph.D, Thomas J.
APPLICANT: Dodge, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADGEMENT-LA Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
273 ACAAGGCCCGAGAACGTATTCA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 ACAAGGCCGAGAACGTATTCA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-923-871C-1/c
; Sequence 1, Application US/07923871C
; Patent No. 5912117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-07-923-871C-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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| Sequence 1, Application PC/TUS9101574
| Sequence 1, Application PC/TUS9101574
| GENERAL INFORMATION:
| APPLICANT: White Ph.D, Thomas J.
| APPLICANT: White Ph.D, Thomas J.
| TITLE OF INVENTION: Method for Diagnosis of Lyme Disease NUMBER OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS: ADDRESSEE: Cetus Corporation | STREET: 1400 Fifty-Third Street | STREET: Ch.D. | STREET: CALLAGORITH | STREET: CALLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 22; DB 2; Length 498; Best Local Similarity 100.0%; Pred. No. 4e-05; Matches 22; Conservative 0; Mismatches 0; Indels
COMPUTER PARAMELE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: ENDORY disk
SCOTTARE: PRESENT PC-DOS/MS-DOS
SCOTTARE: PRESENT NO FORM:
PRING DATE:
PRING DATE:
CLASSIFICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: PRESENCE/DOCKET NUMBER: 8697
TELERBANCE/DOCKET NUMBER: 8697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 ACAAGGCCCGAGAACGTATTCA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (164..165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 498 base pairs TYPE: mucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (35..36)
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complement (167)
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Gaps
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100.0%; Score 22; DB 3; Length 1284;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 445..1063
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATION: 959..1086 JOHER INFORMATION: /note= "Region B - The 3' End of OTHER INFORMATION: Domain I in the 23S rRNA"
US-09-052-333A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Region A - Region of the
Intergenic Spacer"
                                                                             CALT: 0.1504
CAPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RIBANGO, CURTIS P.
REGISTRATION NUMBER: 27,976
REGISTRATION NUMBER: 27,976
RETERPONE: 309/681-658
INFORMATION: TELEFONE: 309/681-658
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1284 base pairs
TYPE: MACHINE CHARACTERISTICS:
LENGTH: 1284 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: FRAN
LOCATION: 1...21
OTHER INFORMATION: /note= "168 rRNA"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 222..44
OTHER INFORMATION: /note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: rrna
LOCATION: 445..1284
OTHER INFORMATION: /note= "235 rRnA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia pneumoniae
STRAIN: CWL-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-052-333A-27/c
; Sequence 27, Application US/09052333A
; Patent No. 6261769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAAGGCCCGAGAACGTATTCA 22
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NAME/KEY: misc RNA
LOCATION: 1..537
OTHER INFORMATION: 7
FEATURE:
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            STATE: LE COUNTRY: US 61604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6261769
TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS: ADDRESSE: Curtis P. Ribando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bam PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01574
FILING DATE: 19910307
CLASSIFICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kaster, Kevin R:
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kaster, Kevin R:
FERENCATION NUMBER: 2536.1
TELEPHONE: (415) 658-5239
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 505 base pairs
TTELEPA: NUCLEIC ACID
STRANDENESS: Single
HOLOGY: linear
MOLOGY: linear
MOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FRATURE:
NAME: NO
FRATURE:
NAME/KEY: UNSUVER: 7-5 A/5)
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1815 N. University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 ACAAGGCCCGAGAACGTATTCA 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (67)
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: complet
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LOCATION:
FEATURE:
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FEATURE:
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LOCATION:
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LOCATION:

PCT-US91-01574-1
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NAME/KEY: misc_RNA
LOCATION: 1.1537
OTHER INFORMATION: /note= "Region A - Region of the
OTHER INFORMATION: Intergenic Spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_RNA
LOCATION: 222.744
OTHER INFORMATION: /note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..221
OTHER INFORMATION: /note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 445..1284
OTHER INFORMATION: /note= "238 rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia pneumoniae
STRAIN: FWL-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: rRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: rRNA
GENERAL INFORMATION:
APPLICANT: Everett, Karin D.E.
APPLICANT: Andersen, Arthur A.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains NUMBER OF SEQUENCE: 73
NUMBER OF SEQUENCE: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: rRNA
LOCATION: 445..1063
COTHER INFORMATION: /note= "Domain I of the 23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_RNA
LOCATION: 1..537
COCATION: NFORMATION: /note= "Region A - Region of the OTHER INFORMATION: Intergenic Spacer"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: rRNA

COCATION: 959..1086

OTHER INFORMATION: /note= "Region B - The 3' End of

OTHER INFORMATION: Domain I in the 238 rRNA"

US-09-052-333A-27
                                                                                                                                                                                                                                                                     COUNTRY: US

ZIATE: IL

COUNTRY: US

ZIP: 61604

COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 0211.97
REGISTRATION NUMBER: 0211.97
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1284 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: rRNA
LOCATION: 445..1284
OTHER INFORMATION: /note= "23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/FEX: . FRNA
LOCATION: .1..221
OTHER INFORMATION: /note= "16S FRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Chlamydia pneumoniae
STRAIN: CWL-1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_RNA
LOCATION: 222.7444
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: rRN
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                               STREET: 1815
CITY: Peoria
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RESULT 7

US-09-052-333A-28/C

US-09-052-333A-28/C

US-09-052-333A-28/C

Sequence 28, Application US/09052333A

Sequence 28, Application US/09052333A

Sequence 28, Application US/09052333A

GENERAL INVENTION:

APPLICANT: Andersen, Arthur A.

TITLE OF INVENTION: Intergenic Spacer Target Sequence for TITLE OF INVENTION: Intergenic Spacer Target Sequence for TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains NUMBER OF SEQUENCES: 73

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ourtis P. Ribando

STREET: 1815 N. University Street

CITY: Peoria

STREET: 18.

COUNTRY: US

ZIP: 616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 445..1063
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CZIF: 6.1604

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: I BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P:
REGISTRATION NUMBER: 27,976
REGISTRATION NUMBER: 27,976
RETERPONE: 309/681-6688
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION: 1284 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: FRNA
MYTT GENCY: NO
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/note= "Domain I of the 23S rRNA"
                                                                                          /note= "23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACAAGGCCCGAGAACGTATTCA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-052-333A-31/c
; Sequence 31, Application US/09052333A
Patent No. 6261769
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RIDAND, CUTLIS P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211
TELECOMUNICATION INFORMATION:
TELEPHONE: 309/681-6688
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1284 base pairs
TYPE: NUCLEIC acid
STRANDENESS: SINGIE
                                                NAME/KEY: rRNA
LOCATION: 445..1284
OTHER INFORMATION: ,
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
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Sequence 29, Application US/09052333A
Patent No. 6261769
GENERAL INFORMATION:
APPLICANT: Everett, Karin D.E.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for
TITLE OF INVENTION: Intergenic Spacer Target Sequence for
Patent No. 6261769
TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street
CITY: Peoria
STATE: 1L
COUMTRY: US
CITY: 61604
                                                                                                                                                                                                         ö
                                                                                                                                                           Query Match 100.0%; Score 22; DB 3; Length 1284; Best Local Similarity 100.0%; Pred. No. 3.9e-05; Matches 22; Conservative 0; Mismatches 0; Indels 0
      ; FEATURE:
; NAME/KEY: rENA
; LOCATION: 959..1086
; OTHER INFORMATION: /note= "Region B - The 3' End of
; OTHER INFORMATION: Domain I in the 23S rENA"
US-09-052-333A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 61604

ZIP: 61604

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: rRNA
LOCATION: 1..221
OTHER INFORMATION: /note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: FRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia pneumoniae
STRAIN: FML-16
FEATURE:
                                                                                                                                                                                                                                                                                 67 ACAAGGCCGAGAACGTATTCA 46
                                                                                                                                                                                                                                                1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: R.Dando, Cutris P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.
TELECOMMUNICATION INFORMATION:
TELEFAX: 309/691-6513
TELEFAX: 309/691-6513
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1284 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_RNA
LOCATION: 222..444
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: rRNA
LOCATION: 445..1063
                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-052-333A-29/c
                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                            g
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APPLICANT: Bverett, Karin D.E.
APPLICANT: Brerett, Karin D.E.
APPLICANT: Andersen, Arthur A.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for
Patent No. 626,749
TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: CALTIS P. Ribando
STREET: 1815 N. University Street
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                 Length 1284;
                                                                                                                                                                                                                                                                                                                                                                  Indels
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 1.537
CHER INFORMATION: /note= "Region A - Region of the OTHER INFORMATION: Intergenic Spacer"
FEATURE:
NAME/KEY: RNA
                                                                                                                                                                                 LOCATION: 959.1086

COTHER INFORMATION: /note= "Region B - The 3' End of CHER INFORMATION: Domain I in the 23S rRNA"

US-09-052-333A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: IL
COUNTRY: US
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/052,333A
FILING DATE:
                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 22; DB 3; I
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0;
```

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GENERAL INFORMATION:
APPLICANT: ABAILAT, CLAUDE
APPLICANT: RABILAT, CLAUDE
APPLICANT: RABILAT,
DIDIER
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: UA
ZIP: 22320
                                                                                                                                                     ö
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                                                                                                                                                     Gaps
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                                                                                                     Length 1408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
                                                                                                100.0%; Score 22; DB 2; I
100.0%; Pred. No. 3.9e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 22; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTATION NUMBER: 30,028
REFERENCE/DOCKET UNHER: WPB 38238
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-277
INPORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1427 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                     1319 ACAAGGCCCGAGAACGTATTCA 1298
                                                                                                                                                                                                                                                                                                                                                                          Sequence 27, Application US/08632470 Patent No. 5976791
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-632-470-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
```

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MABILAT, CLAUDE
APPLICANT: MADULT, DIDIER
TITLE OF INVENTION: NUCLECTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 2; Length 14; Pred. No. 3.9e-05; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PETENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:

REPLICATION NUMBER: US/08/632,470
FILING DATE: 08-UUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

RECISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECHONE: (703)-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 22; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0;
              ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEPAX: (703)-836-6400
TELEPAX: (703)-836-5787
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1432 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1327 ACAAGGCCCGAGAACGTATTCA 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-632-470-34/c
; Sequence 34, Application US/08632470
; Patent No. 5976791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACAAGGCCCGAGAACGTATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1436 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
) MOLECULE TYPE: DNA (genomic)
US-08-632-470-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-632-470-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 1436 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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Sequence 32, Application US/08632470

Patent No. 5976791

GENERAL INPORMATION:
TOTAL OF INVENTION: MUCLECTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: HYBRENGES: 53
CORRESPONDENCE ADDRESS: 53
CORRESPONDENCE ADDRESS: 53
CORRESPECT: P.O. BOX 19928

TITLE OF LINEAANRIA
STREET: P.O. BOX 19928

COUNTRY: USA
COUNTRY: USA
TITLE SADABLE FORM:
MEDIUM TYPE: Floppy disk
OCMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.30
COMPUTER: DATE: US/08/632,470
FILING DATE: 08-UTL-1996
TILING DATE: 08-UTL-1996
TILING DATE: 08-UTL-1996
                                             NUCLECTIDE FRAGMENTS CAPABLE OF
HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
THEIR USE AS PROBES OR PRIMERS
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cuery Match 100.0%; Score 22; DB 2; Length 1432; Best Local Similarity 100.0%; Pred. No. 3.9e-05; Matches 22; Conservative 0; Mismatches 0; Indels (
APPLICANT: RACULT, DIDIER
TITLE OF INVENTION: NUCLECTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSED OLIFK & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STRATE: VG
COUNTRY: UGA
COUNTRY: UGA
ZIP: 22320
COMPUTER: IDEN PC COMPACIBLE
MEDIUM TYPE: Floppy disk
COUNTRY: Patentin Release #1.0, Version #1.30
COUNTRY: Betentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
MEDIUM TYPE: 08-UUL-1996
CURRENT APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-UUL-1996
CLREATING DATE: 08-UUL-1996
CLREATING DATE: 08-UUL-1996
CLREATING DATE: 08-UUL-1996
CLREATING DATE: 08-UUL-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-86-6400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-86-6400
TELEPHONE: (703)-86-6400
TELEPHONE: (703)-86-6400
TELEPHONE: (703)-86-6787
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1432 base pairs
TYPE: nucleic acid
STRAMDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
US-08-632-470-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-632-470-32/c
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1331 ACAAGGCCCGAGAACGTATTCA 1310

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GENERAL INCRMATION:
APPLICANT: MABILAT, CLAUDE
APPLICANT: MASILAT, CLAUDE
APPLICANT: RAGULT, DIDIER
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 22; DB 2; Length 1438;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                   CITXELL
CITXELL
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 2323C
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREFEIT RELEASE #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/632,470
FILIGO DATE: 08-UUL-196
CLASSIFICATION NUMBER: US/08/632,470
FILIGO DATE: WE OB-UUL-196
CLASSIFICATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-5787
INPORMATION POR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: NUMBERS: single
STRANDEDRESS: single
MOLECULE TYPE: DNA (genomic)
US-08-632-470-24

100.0%; SCOIF 22; DB 2; L
RESULT 15
US-08-632-470-24/c
Sequence 24, Application US/08632470
Patent No. 5976791
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1333 ACAAGGCCCGAGAACGTATTCA 1312 1 ACAAGGCCCGAGAACGTATTCA 22 g ò

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Gaps

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Search completed: August 4, 2004, 09:23:29 Job time : 40.759 secs

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US-09-726-774-11
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                                                                                                                     4, 2004, 06:01:54; Search time 36.1446 Seconds (without alignments) 307.073 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     682709 segs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                 ggaggaaggcgaggatgacg
                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                      US-09-940-860-2
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score:

Perfect

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Sequence:

Scoring table:

Searched:

Database

	Description	Sequence 11, Appl	ý	37	(1)	Η	73	13	12	11226,	Sequence 11111, A	10956,	8573,	2, Api	2, Api	7	2, Apr		2,	6286	6365	Sequence 6182, Ap	Sequence 2, Appli	1, 1	6707	13, 7		Sequence 10382, A
SUMMAKIES	ID	US-09-726-774-11	US-09-052-333A-6	US-09-052-333A-37	US-09-198-452A-1	19-252-991A-11	39-252-991A-13	-09-252-991A	-09-252-991A-12	US-09-252-991A-11226	US-09-252-991A-11111	09-252-991A-10	US-09-621-976-8573	38-818-	8-818-111	-60-	-09-072-596	9-072-	US-09-050-739-5	US-09-252-991A-6286	-09-252-991A-636	US-09-252-991A-6182	US-09-103-840A-2	US-09-103-840A-1	-09-252-991A-	US-09-743-207-13	-09-252-9	US-09-252-991A-10382
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*	Query		100.0	100.0	100.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	ď.	75.0	70.0	70.0	ö	70.0
	Score	20	20	20	20	16	16	16	16	16	16	16	15	15	15	15	15	15	15	15	15	15	15	15	14	14	14	14
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                       Sequence 6674, Apple Sequence 211, Appl Sequence 2445, Apple Sequence 6415, Apple Sequence 6411, Appli Sequence 1, Appli Sequence 3, Appli Sequence 91, Appli
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Patent No. 6261769

Patent No. 6261769

Patent No. 6261760

Patent No. 10204 Application US/09052333A

GENERAL INFORMATION:

APPLICANT: Patent Arthur A.

TITLE OF INVENTION: Intergenic Spacer Target Sequence for TITLE OF INVENTION: Intergenic Spacer Target Sequence for TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis P. Ribando

STREET: 1815 N. University Street

CITY: Pecria

STATE: IL

CONNTR: US

ZIP: 61604

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sequence 1.6 Application US/09726774

Patent No. 1677153

GENERAL INFORMATION:
TITLE OF INVENTION: Patrick L.
TITLE OF INVENTION: Composition
TITLE OF INVENTION: Composition
FILE REFERENCE: 045-0032.30

CURRENT APPLICATION NUMBER: US/09/726,774

CURRENT PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

NUMBER OF SEQ ID NOS: 139

SEQ ID NO 11

LENGTH: 1548

LENGTH: 1548
US-09-489-039A-4798
US-09-522-91A-6674
US-09-673-395A-11
US-09-252-91A-2607
US-09-252-91A-245
US-09-252-91A-10268
US-09-252-91A-10268
US-09-252-991A-10268
US-09-252-991A-10268
US-09-252-991A-10268
US-09-252-991A-10268
US-08-888-651-3
US-08-888-651-3
US-08-888-651-3
US-08-813-819-3
US-09-920-048-3
US-09-920-048-3
US-10-060-332-3
US-10-060-332-3
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Best Local Similarity 100.0%; P.
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-726-774-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-052-333A-6
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 803..1424
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 1320..1447
; OTHER INFORMATION: /note= "Region B - The 3' End of ; OTHER INFORMATION: Domain I in the 23S rRNA" US-09-052-333A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "Region A - Region of the OTHER INFORMATION: Intergenic Spacer"
                                                                                      CITY: Peoria
CITY: Peoria
CUNTRY: IL
COUNTRY: IL
COUNTRY: IL
COUNTRY: E16.04
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_RNA.
LOCATION: 565..802
OTHER INFORMATION: /note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: rRNA
LOCATION: 1..564
OTHER INFORMATION: /note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: rRNA
LOCATION: 803..2762
OTHER INFORMATION: /note= "23S rRNA"
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street
CITY: Peoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: TRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
CANGINAL SOURCE:
ORGANISM: Chlamydia trachomatis
STRAIN: R22
                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 309/681-668
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 2762 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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NAME/KEY: misc_RNA
LOCATION: 346..895
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/09052333A
Patent No. 6561769
CENERAL INFORMATION:
APPLICANT: Everet, Karin D.E.
APPLICANT: Andersen, Arthur A.
FITLE OF INVENTION: Intergenic Spacer Target Sequence for Patent No. 6561769
TITLE OF INVENTION: Detecting and Distinguishing Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: rRNA
LOCATION: 789..1409
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_RNA
LOCATION: 346.7881
OTHER INFORMATION: /note= "Region A - Region of the
OTHER INFORMATION: Intergenic Spacer"
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1303..1432
OTHER INFORMATION: /note= "Region B - The 3' End of corner information: Domain I in the 23S rRNA"
US-09-052-333A-6
                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: FRNA
LOCATION: 1..564
OTHER INFORMATION: /note= "16S FRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 769..2751
OTHER INFORMATION: /note= "23S rRNA"
                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.97
TELECOMUNICATION INFORMATION:
TELEPHONE: 309/681-6513
TELEFAX: 309/681-6588
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2751 base pairs
TYPE: nucleic acid
STRANDENRES: single
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia psittaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 GGAGGAAGGCGAGGATGACG 212
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LOCATION: 565.788
OTHER INFORMATION:
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LOCATION: 789.
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US-09-052-333A-37
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193 GGAGGAAGGCGAGGATGACG 212

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Detecting and Distinguishing Chlamydial Strains

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LOCATION: (270001)...(285000)

OTHER INFORMATION: n=a or c or g or t name/ceture
LOCATION: (285001)...(300000)

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LOCATION: (300001)...(315000)

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LOCATION: (315001)...(33000)

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LOCATION: (315001)...(33000)

OTHER INFORMATION: n=a or c or g or t name/cety: misc feature
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LOCATION: (345001)...(36000)

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LOCATION: (330001)...(39000)

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LOCATION: (330001)...(39000)

OTHER INFORMATION: n=a or c or g or t
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THEN INFORMATION: n=a or c or g or t WE/KEY: MISC Feature CATION: (456001). (460000)

THEN INFORMATION: n=a or c or g or t WE/KEY: MISC Feature CATION: n=a or c or g or t WE/KEY: MISC Feature CATION: (495000). (495001). (495001). (495001). (495001). (495001). (495001). (495001). (495001). (495001). (495001). (495001).
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LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEX: misc_feature
LOCATION: (630001)..(645000)
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IION: (435001)..(450000)
R INFORMATION: n=a or c or g or
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LOCATION: (58501)..(60000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
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LOCATION: (510\(\tilde{0}\)011. (52500)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or
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NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
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LOCATION: (40501)...(42000)
OTHER INFORMATION: n=a or c or g
LOCATION: (420001)...(43500)
OTHER INFORMATION: n=a or c or g
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LOCATION: (600001)..(615000)
JTHER INFORMATION: n=a or c or g
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TION: (390001)..(405000)
INFORMATION: n=a or c or g
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ION: (49501)..(510000)
INFORMATION: n=a or c or g
                                                                                                                                                       APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WAME/KEY: misc feature
LOCATION: (75001)..(90000)
JTHER INFORMATION: n=a or c or g or t
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LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc_feature
LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAME/KET: misc feature
LOCATION: (1)...(15000)
OTHER INFORMATION: n=a or c or g or
NAME/KET: misc feature
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OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or
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LOCATION: (225001)..(240000)
OTHER INFORMATION: n=a or c or g or
                                                                  Sequence 1, Application US/09198452A Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (15001)...(16500)
OTHER INFORMATION: n=a or c or g
NAMEKEY: misc_feature
LOCATION: (16501)...(18000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c or g
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COGATION: (255001)..(270000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Chlamydia pneumoniae
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            RESULT 4
US-09-198-452A-1
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

ATTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENDE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 1107
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SEQUENCE 13193, Application US/09252991A
SEQUENCE 551795
SEQUENCE 13193, Application US/09252991A
SEQUENCE SESTIFE
SERVERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUMBER: US/09/252,991A
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13193
LENGTH: 1179
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  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 16; DB 4; Length 1107; 100.0%; Pred. No. 2.4;
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                  FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                   100.0%; Prea. ...
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                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
// ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13336
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Best Local Similarity 100.
Matches 16; Conservative
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10.5-09-10.29
Sequence 110.29, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
ITTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (66001)..(675000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (675001)..(690000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                        LOCATION: (705501)...(72000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (720001)...(73500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (735001)...(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (735001)...(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (750001)...(76500)
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LOCATION: (765001)..(780000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (88501)..(900000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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LOCATION: (690001)..(705000)
OTHER INFORMATION: n=a or c or g or
OTHER INFORMATION: n=a or c or g or
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Sequence 11111, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: MUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11111
: LENGTH: 1974
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APPLICANT:
MATC J. RUDEHFIELD ALD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10956
LENGTH: 2283
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; Sequence 8573, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Globert, S.
; APPLICANT: Globert, S.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
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100.0%; Pred. No. 2.4;
:ive 0; Mismatches
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ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 100.
Matches 16; Conservative
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US-09-252-991A-10956
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US-09-621-976-8573/c
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 09/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11226
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12614

LENGTH: 1308
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Pred. No. 2.4;
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Sequence 12614, Application US/09252991A
Patent No. 6551795
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Sequence 11226, Application US/09252991A
Patent No. 6551795
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100.0%; Pro
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13193
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 100.
Matches 16; Conservative
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ABOURESEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF VOMBER OF SEQUENCES: 148
CORRESPONDENCES: 148
CORRESPONDENCES: SEED and BERRY LLP
ADDRESSEE: SEED and BERRY LLP
CITY: Seattle
CITY: Seattle
STREET: 6300 Columbia Center, 701 Fifth Avenue
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.0%; Score 15; DB 4; Length 752; Best Local Similarity 100.0%; Pred. No. 8.5; Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                             434 AAGGCGAGGATGACG 448
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
ALTILE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                         75.0%; Score 15; DB 4; Length 191; 100.0%; Pred. No. 8.7; tive 0; Mismatches 0; Indels
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MM-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 42
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERRING-DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
               CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 8573
LENGTH: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
                                                                                                                                                                                                NAME/KEY: misc_feature; LOCATION: 2; OTHER INFORMATION: n=a, g, c or t US-09-621-976-8573
                                                                                                                                                                                                                                                                                                                                                                                                                               188 GGAGGAAGGCGAGGA 174
FILE REFERENCE: GENSET.054PR2
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 15; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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US-08-818-112-2
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CITY: Seattle

STATE: Washington

COUNTRY: Washington

COUNTRY: Washington

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IRM PC compatible

COMPUTER: IRM PC compuTER: IRM PC compatible

COMPUTER: IRM PC
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Search completed: August 4, 2004, 09:23:28 Job time: 42.1446 secs

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Query Match
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US-09-940-860-4
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Sequence 78545, A
Sequence 27667, A
Sequence 1484, Ap
Sequence 3179, Ap
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Sequence 35039, A
Sequence 1280, Ap
Sequence 352, App
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31366, A
1477, Ap
1478, Ap
1475, Ap
                                                                                                                                                                                                                                                August 4, 2004, 07:44:29; Search time 190.012 Seconds (without alignments) 541.892 Million cell updates/sec
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1. (cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

1. (cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

2. (cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

2. (cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

2. (cgn2_6/ptodata/2/pubpna/DS07_NEW PUB.seq:*

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3. (cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

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3. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3. (cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

4. (cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

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5. (cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-437-965-78545
US-10-169-493-27667
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US-10-021-32-3179
US-09-919-197-10
US-10-425-114-3639
US-09-854-867-352
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Sequence	Sequenc	Sequenc	Sequenc	Sequenc	Seguena	Seguenc	Seguenc	Seguenc	Sequenc	Sequenc	Sequenc	Seguenc	Sequenc	Seguenc	Sequenc	Sequenc	Seguenc	Seguenc	Seguenc	Seguenc	Seguenc	Seguenc	Seguenc	Seguenc	Seguenc	Seguenc	Seguenc	Sequence	Seguenc
53-4 63-4	-10-027-632-137	-10-027-632-13774	-10-027-632-137	-10-027-632-13774	-10-027-632-137	-10-027-632-13774	-09-535-459-148	-10-424-599-124	-10-021-323-341	-10-027-632-2156	-10-027-632-215	-10-027-632-2156	-10-027-632-2156	-10-333-184-52	-10-437-963-70931	-10-027-632-16488	-10-027-632-16	-10-027-632-16488	-10-027-632-16488	-10-027-632-16488	0-027-632-16488	-10-152-319A-204	-10-425-114-1222	-10-425-114-1665	-10-389-647-21	-10-282-122A-337	-10-369-493-345	-10-425-114-1750	0-408-167A-
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Sequence 4, Application US/09940860; Sequence 4, Application US/09940860; Publication No. US2004000555811; GRENRAL INFORMATION: GRENRAL INFORMATION: GRENRAL TROCHMEN, Richard APPLICAMT: Rothman, Maulik TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA; FILE REFERENCE: 01107.00185; CURRENT APPLICATION NUMBER: US/09/940,860; CURRENT APPLICATION NUMBER: 06/229; PRIOR APPLICATION NUMBER: 60/229; PRIOR APPLICATION NUMBER: 60/229; PRIOR FILING DATE: 2001-08-31; NUMBER OF SEQ ID NOS: 7; SEQ ID NO 4; SEQ ID NO 4; SEQ ID NO 4; LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: synthetic amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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Gaps

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Indels

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0; Mismatches

21; Conservative

100.0%; Score 21; DB 11; Length 21; 100.0%; Pred. No. 0.02;

RESULT 2
US-10-437-963-78545/c
Sequence 78545, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

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APPLICANT: Mullahy, Sara J.

APPLICANT: Mullahy, Rebecca E.

APPLICANT: Naughton. PolyNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE FILE REPERENCE: PD-1014 CIP
CURRENT APPLICATION NUMBER: US/09/535,459
CURRENT PILLING DATE: 2000-03-24
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2170
SOFTWARE: PERL Program
SEQ ID NO 1484
LENGTH: 407
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APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
FILE REFERENCE: ISPH-0593
CURRENT APPLICATION NUMBER: US/09/919,197
UNDMBER OF SEQ ID NOS: 89
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APPLICANT: Peng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd C.C.
APPLICANT: Ziegler, Todd C.C.
APPLICANT: Ziegler, Todd C.C.
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US/10/255, 619
PRIOR APPLICATION NUMBER: US/200-12-14
NUMBER OF SEQ ID NOS: 17880
LENGTH: 600
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                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01212406
US-09-535-459-1484
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 407
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, OTHER INFORMATION: Clone ID: LIB3825-023-Q6-K6-G3
US-10-021-323-3179
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100.0%; Pred. No. 13;
iive 0; Mismatches 0;
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Publication No. US20030083484A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGCCAGCAGCAGCGGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 16; Conserva
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US-09-919-197-10
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                                                                                                                                                                                                 and Other Molecules Associated With
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Warnfession of MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE REFERENCE: 38-10(52052)B
TITLE OF INVENTION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27667
LENGTH: 3502
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81.0%; Score 17; DB 17; Length 1980;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 17; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 16; Length 3502;
Pred. No. 3.5;
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                                                                                                                                            APPLICANT: Barbaruk, Brad APPLICANT: Barbaruk, Brad APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Oth TITLE OF INVENTION: Plants and Uses Thereof for Plant FILE REFERENCE: 38-21 [5322] B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT PILLING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 LENGTH: 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78341C.1
US-10-437-963-78545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 27667, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
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La Rosa, Thomas J.

Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wei
Boubharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1018 CAGCAGCAGCGGTAATA 1002
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Best Local Similarity 100.0%; P. Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 CAGCAGCAGCGGTAATA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-369-493-27667
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
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US-09-535-459-1484
                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Sequence 352, Application US/09854867
Sequence 352, Application US/09854867
Publication No. US20030224356A1
GENERAL INFORMATION:
GENERAL INFORMATION:
THE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING THE REPRENCE: 3030 THE REPRENCE: 3030 THE CURRENT APPLICATION UNMBER: US/09/854,867
CURRENT APPLICATION UNMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: Patentin version 3.1
IERIGIH: 1992
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                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_101161C.1
US-10-437-963-1280
                                                                FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1837)
OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                  1403 GTGCCAGCAGCAGCGG 1388
                                                                                                                                                                                                                                                                                                                                       1 GTGCCAGCAGCAGCGG 16
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LOCATION: (1)..(1992)
OTHER INFORMATION: 11pa15_5
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LOCATION: (1558)..(1558)
OTHER INFORMATION: n is a,
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; LOCATION: (1802)...(1802)
; OTHER INFORMATION: n is a,
US-09-854-867-352
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OTHER INFORMATION: n is a,
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LOCATION: (1149)..(1149)
OTHER INFORMATION: n is a,
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LOCATION: (1418)..(1418)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (1533)..(1533)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is
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ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
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LOCATION: (1261)..(126
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Matches 16; Conserve
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zoo, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: W. Wei
APPLICANT: Buukharcu, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Paing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 1280
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...rlcant Edou, Yihua
APPLICANT Kovalic, David K.
APPLICANT Screen, Steven E
APPLICANT Tabaska, Jack E
APPLICANT Tabaska, Jack E
APPLICANT Tabaska, Jack E
APPLICANT Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 35039
LENGTH: 1350
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red. No. 13;
Mismatches 0; Indels
                                                                                                                                                                                                                        DB 10; Length 1119; 13;
                                                                                                                                                                                                                                                                       0; Indels
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COTHER INFORMATION: Clone ID: UC-ZMFL/TEOSIN/TE032D03_FLIUS-10-425-114-35039
                                                                                                                                                                                                                                                                   Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10 LENGTH: 1119
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Best Local Similarity 100.0%; Pred. No.
Matches 16; Conservative 0; Mismatci
                                                                                                                                                                                                                        Query Match 76.2%; Score 16; Best Local Similarity 100.0%; Pred. No. Matches 16; Conservative 0; Mismatc
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Publication No. US20040123343A1
GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mexicana
                                                                                                                                                                                                                                                                                                                                                 161 GTGCCAGCAGCAG 176
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                                                                    TYPE: DNA
ORGANISM: Mus musculus
                                                                                                          ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)...(815)
US-09-919-197-10
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Sequence 1477, Application US/09535459
Publication No. US20030040615A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Naug
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                 PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 3001-03-16
PRIOR PILING DATE: 3001-03-16
PRIOR PILING DATE: 3001-03-16
PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 3001-03-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.4%; Score 15; DB 10; Length 280; 100.0%; Pred. No. 48; ive 0; Mismatches 0; Indels
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) OTHER INFORMATION: Incyte ID No. US20030040615A1 hu00988392

US-09-535-459-1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Stuan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTGCCAGCAGCGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 gccagcagcagcagr 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) TYPE: DNA
; ORGANISM: Pseudomonas putida
US-10-282-122A-31366
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ORGANISM: Homo sapiens
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Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 15; Conserv
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US-09-535-459-1477/c
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0; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-6

PRIOR PILING DATE: 2000-05-6
0; Mismatches
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US-10-425-114-1420
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PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                         1317 GTGCCAGCAGCAG 1302
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                             1 GTGCCAGCAGCAGCGG 16
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 100.
Matches 16; Conservative
16; Conservative
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TITLE OF INVENTION: POLYNUCLECTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECUL: FILE REFERENCE: PD-1014 CIP COURENT APPLICATION NUMBER: US/09/535,459
CURRENT APPLICATION NUMBER: 2000-03-24
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2170
SOFTWARE: PERL Program
SEQ ID NO 1479
LENGTH: 391
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Note: National Control of Control 
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-354-4975, Application US/09535459

Sequence 1475, Application US/09535459

Publication No. US20030040615A1

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Seilhamer, Angelo M.

APPLICANT: Stuara L.

APPLICANT: Mullahy, Sara J.

APPLICANT: Stuara J.

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APPLICANT: Mullahy, Sara J.

APPLICANT: Stuara J.

APPLICANT: Mullahy, Sara J.

APPL
ug-09-940-86

"ITLE OF INVENTION: POLYNUCLECTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
CURRENT APPLICATION NUMBER: US/09/535,459
CURRENT FILING DATE: 2000-03-24
Prior application data removed - consult PALM or file wrapper
SOFTWARE: PERL Program
SEQ ID NO 1478
LENGTH: 296
TYPE: NAT
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US-09-535-459-1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01006476
US-09-535-459-1478
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US-09-535-459-1479/c
Sequence 1479, Application US/09535459
Publication No. US20030040615A1
GENERAL INFORMATION:
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APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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9: geneseqn20s:*
10: geneseqn2004s:*
10: geneseqn2004s:*

Post-processing: Listing first 45 summaries

Database :

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ACA45835	AAV02903	AAA98876	AAA98158	AAD29987	ABL17969	ABQ77568	AAX22772	AAX22778	AAV29137	ACC44418	ACA47979	AAZ20095	AAH17305	ADB63487	AAZ98625	AAZ20096	ABL07099	ABL28180	ABT06279	ABT06280	ADD78281	
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ALIGNMENTS

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This is the nucleotide sequence of one strand of the PSI-PL470 gene of the 30.7 kb extrachromosomal plastid of Plasmodium berghei. This plastid encodes organelle-like rRNAs, trbosomal proteins and RNA polymerase subunits, amongst others. Plasmodium is detected in a human or animal sample by treating it, or derived nucleic acid, with a Plasmodium extrachromosomal genetic element or derived nucleic acid (A) and detecting any hybridisation. (A) can include the PSI-PL470, PLH-PPH, PRB
                                                                                                                                              Malaria; infection; therapy; diagnosis; vaccine; plastid; PS1-PL470 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting Plasmodium infection from hybridisation with extrachromosomal element - providing genus or species specific diagnosis with few false negatives, in humans or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                  Tan TMC;
                                                                                                                                                                                                                                                                                                                                                                                                                  Nelson JS,
                                                                                                                  Plasmodium berghei plastid PS1-PL470 gene.
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(MOLE-) INST MOLECULAR & CELL BIOLOGY.
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            AAV33135 standard; DNA; 5849 BP.
                                                                                                                                                                                          Plasmodium berghei; ANKA strain.
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97AU-00006329.
97AU-00009481.
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21-APR-1997;
26-SEP-1997;
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                                                                      17-OCT-2003
07-DEC-1998
                                                                                                                                                                                                                                                    13-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                    Kara AKU,
                                          AAV33135;
AAV33135
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Neisseria meningitidis, Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.

Neisseria gonorrhoeae.

W09924578-A2

Neisseria gonorrhoeae complete ORF139 sequence.

(first entry)

08-OCT-1999

AAZ12223

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RESULT 3 AAZ12223/c ID AAZ12223 standard; DNA; 1542

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             or PWQ gene, the mitochondrial coxI gene, and nucleic acids derived from them. Also new are (A)-specific probes and primers (see AAV3119-56). The method is used to diagnose Plasmodium infection. Also (not claimed) the polypeptides encoded by (A) are useful as targets for drug development and for development of anti-malaria vaccines. The high degree of similarity between (A) from different species allows development of genus con species-specific assays that result in fewer false negatives than known methods (typically 1% against 3%). (Updated on 17-OCT-2003 to standardise OS field)
and nucleic acids derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
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medicament for treating or preventing N. gonorrheae infection
                                                                                                                                                                            Sequence 5849 BP; 2296 A; 673 C; 557 G; 2323 T; 0 U; 0 Other;
                                                                                                                                                                                                          Score 21; DB 2; Length 5849;
Pred. No. 0.44;
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Pred. No. 37;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                               0; Mismatches
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100.0%; Pre
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Best Local Similarity 100.
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Best Local Similarity
Matches 17; Conserv
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Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorthoese which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their mucleic acids and antibodies are used for diagnosis prevention (as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                             Proteins from Neisseria meningitidis and N. gonorrhoeae useful diagnosis, treatment and prevention of infection.
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Pred. No.
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Best Local Similarity 100.
Matches 17; Conservative
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27-NOV-1997;
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P-PSDB; ABB65459.
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(PEKE ) PE CORP NY
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                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 23168
Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3593 BP; 1055 A; 1047 C; 919 G; 572 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 23171; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      81.0%; Score 17; DB 4; Length 3593; 100.0%; Pred. No. 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TGCCAGCAGCAGCGGTA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL09562 standard; cDNA; 6161
                                                                                                                                                                  Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.0%;
nes 17; Conservative 0
                                                                                                              23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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2000US-00614150.
                                                                                          23-MAR-2001; 2001WO-US009231
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        pharmaceutical; gene; ss
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                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                 Adams M,
                                                                                                                                                                                    WPI; 2001-656860/75.
P-PSDB; ABB65460.
                                                                                                                                             (PEKE ) PE CORP NY
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                                                WO200171042-A2
                                                                                                                                                                                                                                         interactions
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila;
                                                                       27-SEP-2001
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.ell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical furge. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-BBR202075). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated Acinetobacter baumannii nucleic acids.
                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial; vaccine; plant biocontrol agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6161 BP; 1747 A; 1568 C; 1438 G; 1408 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 23168; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 4;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
Myers EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; SEQ ID NO 2320; 328pp; English.
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100.0%; Pre
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PWD,
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Best Local Similarity 100.
Matches 17; Conservative
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The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; ds; gene; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                              76.2%; Score 16; DB 8; Length 684; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                           Sequence 684 BP; 203 A; 127 C; 159 G; 195 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat gene X62660, SEQ ID NO 9802.
                                                                                                                                                                                                                                                                                                                                                                                                                                ADE63858 standard; DNA; 804 BP.
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                                                                                                                                                                                                                                                                                                                              170 cadcadcadcadraar 185
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                            5 CAGCAGCAGCGGTAAT 20
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                                                                                                                                                                                                                                                       16, Conservative
                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE63858;
                                                                                                                                             protein.
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method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat DNA (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal
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                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; ds; gene; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                        Sequence 804 BP; 261 A; 178 C; 198 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                          Score 16; DB 9; Length 804;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                 0; Indels
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100.0%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD48493 standard; DNA; 804 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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                                                                                                                                                                                                                                                                                                                                                                                         1 GTGCCAGCAGCAGCGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                              92 graccagcagcagcg 77
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Best Local Similarity 100.
Matches 16; Conservative
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GENBANK; X62660.
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subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition computisng the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (CNI) in an animal (e.g. gene therapy). The sequence presented is a rat DNA (shown in Table 2 of the specification) which encodes one of the polypeptides of the invention which is differentially expressed during pain. Note: The sequence data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
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Sequence 804 BP; 261 A; 178 C; 198 G; 167 T; 0 U; 0 Other;

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Gaps
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76.2%; Score 16; DB 9; Length 804; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                      GIGCCAGCAGCAGCGG 16
                                                                            GTGCCAGCAGCAGCGG 77
               Local Similarity 100.
ses 16; Conservative
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    Query Match
                Best Loc
Matches
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Antiarteriosclerotic, cardiant, vasotropic, antiinfective, cytostatic, antiinflammatory, inhibitor; antisense gene therapy, atherosclerosis; short heterodimer partner-1; abnormal; lipid; cholesterol metabolism; cardiovascular disease; infection; inflammation; tumour formation; mouse; Short heterodimer partner-1 expression mouse DNA SEQ ID No 10. ABT34135 standard; DNA; 1119 BP. (first entry) 12-JUN-2003 ABT34135; RESULT 9 ABT34135

17-JUL-2002; 2002WO-US023245 31-JUL-2001; 2001US-00919197 (ISIS-) ISIS PHARM INC. Graham MJ; WPI; 2003-248161/24. P-PSDB; AAO27109. 13-FEB-2003. Crooke RM,

WO2003012033-A2 Mus musculus

murine; ds.

New antisense oligonucleotide targeted to a nucleic acid encoding short heterodimer partner-1, useful for treating diseases involving abnormal lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular diseases

Example 9; Page 103-105; 121pp; English.

The invention relates to a novel compound of 8 - 50 nucleobases in length targeted to a nucleic acid molecule encoding a short heterodimer partner-

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I. The novel compound specifically hybridizes with a nucleic acid molecule encoding the short heterodimer partner-1, and inhibits the expression of the nucleic acid molecule. The compound, and a composition comprising it are useful for treating a disease or condition associated with the short heterodimer partner-1, particularly a condition involving abnormal lipid or cholesterol metabolism such as atherosclerosis or a cardiovascular disease. They are also useful in research and diagnostics for modulating the expression of short heterodimer partner-1. They can also be useful prophylactically in preventing or delaying infection, inflammation or tumour formation. This polynucleotide represents a mouse DNA sequence relating to the short heterodimer partner-1 of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                 Length 1119;
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                                                                                                                                                                                                                                                                           Score 16; DB 7; Length 111
Pred. No. 1.1e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                     76.50
100.08; Li
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                                                                                                                                                                                                                                                                                                                                                                                    161 GTGCCAGCAGCAGCGG 176
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                     Local Similarity 100.
tes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL11243;
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL11243
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid controlled whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation of an adentifying a gene required for cellular proliferation of the biological pathway in which a proliferation required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a compound; a compound; a cutivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to an isolated nucleic acid comprising any one of
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prokaryotic essential gene; cell proliferation;
                            Length 2854;
DB 4; Le...
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haselbeck R,
Yamamoto R,
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; SEQ ID NO 31366; 1766pp; English.
                        76.2%; Score 16;
100.0%; Pred. No.
ive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prokaryotic essential gene #25153.
                                                                                                                                                                                                                                                                                                                                                                                                   ACA43496 standard; DNA; 3672 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malone C,
Carr GJ,
                                                                                                                                                                                                          2354 CCAGCAGCAGCGGTAA 2369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0049231P.
08-FEB-2002; 2002US-00372881.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002WO-US009107
                                                                                                                                                                4 CCAGCAGCAGCGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2003 (first entry)
                                                                                            16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zamudio C,
Trawick JD,
                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug design; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABU39626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA43496;
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Wall D,
                                                                                        Matches
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for cellular proliferation to isolate candidate molecules for rational dary discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. arreus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryoric essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide SEQ ID NO 28208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5471 BP; 1481 A; 1326 C; 1238 G; 1426 T; 0 U; 0 Other;
                                                                                                                                                                       Sequence 3672 BP; 660 A; 1207 C; 1179 G; 626 T; 0 U; 0 Other;
                                                                                                                                                                                                          Length 3672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 28208; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                        76.2%; Score 16; DB 7; Le
100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0;
                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                    3545 Gráccadcadcaded 3560
                                                                                                                                                                                                                                                                                                                                                                                                            ABL11242 standard; cDNA; 5471
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                   1 GTGCCAGCAGCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABB67139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL11242;
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Gaps

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76.2%; Score 16; DB 4; Length 5471; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100.0 Matches 16; Conservative

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WO2003020741-A1.
                                                                                                                                                                                 Fu S,
                                                          WO200061738-A2
                                 Gallus gallus.
                                                                                                                                  .2-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD17780;
                                                                                                                                                                                Vogt PK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to deoxyribonuclease (DLAD) proteins and coding sequences, (see AAP60715-6 and AAB72416-7). DLAD is an endonuclease and is capable of divalent cation-independent cleavage of DNA under acidic conditions. DLAD can be used as a substitute for DNAse I in treating cystic fibrosis, and is useful in the prevention and treatment of infectious diseases. The present sequence is a PCR primer for murine DLAD signal peptide (AAP60715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viral Jun; v-Jun; cellular Jun; c-Jun; immune system disorder; haematopoietic cell disorder; autoimmune disorder; allergy; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                Acidic deoxyribonuclease capable of divalent cation-independent cleavage of DNA under acidic even neutral pH and not inhibited by G-actin, useful in remedies for cystic fibrosis and for treatment of infectious diseases
                                                                                                                                                                                              Murine; DNase; DLAD; deoxyribonuclease; endonuclease; cystic fibrosis; infectious disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone VGT18 of a gene that is differentially regulated by viral Jun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.4%; Score 15; DB 4; Length 32; 100.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32 BP; 5 A; 13 C; 8 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Prec. ...
                                                                                                                                                                         Murine DLAD signal peptide PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 29; 61pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC61717 standard; DNA; 130 BP.
                                3971 CCAGCAGCAGCAGTAA 3986
                                                                                                 BP
                                                                                                                                                                                                                                                                                                          01-MAY-2000; 2000WO-JP002893
                                                                                                                                                                                                                                                                                                                                    99JP-00230870
              4 CCAGCAGCAGCGGTAA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TGCCAGCAGCAGCGG 16
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(first entry)
                                                                                       723/c
AAF60723 standard; DNA; 32
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-218348/22.
                                                                                                                                                                                                                                                                                                                                                                                   Shiokawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            (TANU/) TANUMA S.
                                                                                                                                                                                                                                                           WO200112793-A1
                                                                                                                                                                                                                                                                                                                                    17-AUG-1999;
                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003
06-MAR-2001
                                                                                                                                                  03-MAY-2001
                                                                                                                                                                                                                                                                                    22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                     ranuma S,
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                                                                                                                         AAF60723;
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Matches
                                                                                   AAF60723/
ID AAF6
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The present sequence is derived from a gene that is differentially regulated by viral Jun (v-Jun) and cellular Jun (c-Jun). The polymucleotide is used to prevent, treat or ameliorate a medical condition, e.g. deficiencies or disorders of the immune system, of haemacopoietic cells, autoimmune disorders, allergic conditions, organ rejection or graft-versus-host-disease, inflammation, hyperproliferative disorders, bacterial, fungal, parasitic and virus infections. It can also be used to modulate hemostatic or thrombolytic activity, regenerate tissues, increase chemostatic or thrombolytic activity, regenerate metabolism, change the physical or mental state of a mammal and can be used as food additives to increase or decrease storage capabilities and nutritional components. (Updated on 15-SEP-2003 to standardise OS field)
organ rejection, graft-versus-host-disease, hyperproliferative disorder;
infection, food additive, storage capability; nutritional component; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; visual phenotype; plant; architecture; leaf surface; chlorotic; bleaching; etching; wet leaf; stunting; elongation; texture; agronomic trait; growth regulation; dwarf variety; insect resistance; heat stress; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules from Gallus domesticus are used for diagnosis and treatment of medial conditions in mammals \varepsilon.g. cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (SeqID 1848) that confers an altered visual phenotype in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dickerson JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 130 BP; 40 A; 37 C; 30 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bottoli ILC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 92; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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                                                                                                                                                                                                                                                                                                                                                12-APR-2000; 2000WO-US009766.
                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0128887P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hilbush BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD17780 standard; DNA; 197
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(DOWC) DOW CHEM CO. (DOWC) DOW AGROSCIENCES LLC.

Ruegger M, Larrinua I, Shukla V; Crosley R, Skokut T,

WPI; 2003-300858/29.

Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for conferring altered visual phenotypes in plants.

Claim 1; SEQ ID NO 1848; 517pp; English.

This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed sensescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual penerating transgenic plant seeds, plant tissues and plant cells containing the polymucleotides described herein. This polymucleotide is a homologue of a DNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.

Sequence 197' BP; 46 A; 66 C; 42 G; 43 T; 0 U; 0 Other;

Query Match 71.4%; Score 15; DB 9; Length 197; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels

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Gaps ; 0

3 GCCAGCAGCAGCGGT 17

74 GCCAGCAGCAGCGGT 60 Š g Search completed: August 4, 2004, 06:43:39 Job time : 174.554 secs

AZ677920 ENTHX83TR CB832595 SWWDmfCAV

score:

Title: Perfect

Sequence:

1

OM nucleic

Run on:

Scoring table:

Word size :

Database

Result No. υ

Searched:

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Surlactorical metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Juliangara, Julia
                                                 AU007074 AU007074
BG623306 GGH6375.3
AA695154 GM03726.3
AM940266 GH06375.3
AM940266 GH07623.3
AM940266 GH07623.3
AM940266 GH07623.3
AM931275 RCS-BT037
A1397756 NCC5HBT3
CD873121 AZO2.122G
BMS 84191 170006872
CC539904 CT240 420
AZ124708 OSJNBD0079P
CC649995 NDL.121H1
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CC649995 NDL.121H1
CC649995 NDL.121H1
CC649995 NDL.121H1
AZ03195 FGAS01172
CC33904 CT34 AD60049P
CC345995 NDL.121H1
BU598465 AGBNCOURT
AZ269457 RPCT-23-4
BB589921 BB569921
BB604685 BB604685
AW866950 CM3-SN003
BU648979 1112075A1
BB736251 BY36525
BY375272 BY775272
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BY375311 BAN0CU32TF
BY769231 BY769221
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                    AU010207 AU010207
CK107208 UB49DPG02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dr. Sergio Verjovski-Almeida
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22879926
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CKZ03195
CKZ03195
CKZ081282
CA581282
CNSO0ZBC
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BY256251
BY275522
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                                      CK107208
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SOURCE
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CG745724 P038-3-H1
B1936798 dc89d01.x
BE517377 WHE0625_B
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                                                                                                     August 4, 2004, 05:41:25; Search time 1462.92 Seconds (without alignments) 428.668 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Unpublished (1997)
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Best Local Similarity 100.
Matches 20; Conservative
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TITLE
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COMMENT
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Pristionchus pacificus
Pristionchus pacificus
Pristionchus pacificus
Nedaryota, Metazoa, Nematoda, Chromadorea; Diplogasterida;
Neodiplogasteridae, Pristionchus.
1 (bases 1 to 1128)
Srinivasa, 1, 51128)
Srinivasa, 1, van der Meulen, M. and Sommer, R.J.
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1128 bp DNA linear GSS 24-OCT-2003
P038-3-H12.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,
GRABETO SURVEY SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                             Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MC1-00357-R100 row: 10 column: D.
                                               SP,
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/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genemic DNA with EcoRI and cloning into the BAC vector."
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 14; Length 420; 100.0%; Pred. No. 7.3; ive 0; Mismatches 0; Indels
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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22835951
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="cercaria"
|Jab_host="Biomphalaria glabrata"
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|/note="Vector: pGEM T-easy"
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db_xref="taxon:6183"

Clone="MC1-0035T-R100-D10.G"

/sex="mixed pool"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: BAC ends.
Location/Qualifiers
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FEATURES

ORIGIN

TITLE

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de89d01.x1 NICHD XGC CO1 Xenopus laevis cDNA clone IMAGE:3404257 3' similar to TR:014597 014597 NON-FUNCTIONAL FOLATE BINDING PROTEIN. i, mRNA sequence. B1936798 1 G1:16251270
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINL at: info@image.llnl.gov
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WHE0625 B06 C11ZA Wheat ABA-treated embryo cDNA library Triticum aestivum cDNA clone WHE0625_B06_C11, mRNA sequence.
BE517377
BE517377.1 GI:9741407
Triticum aestivum (bread wheat)
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/lab host."DH10B (phage-resistant)"
/lab host."DH10B (phage-resistant)"
/loone lib="NICHD XGC_OOI"
/note="Vector: pcWv-SDR76; Site 1: Not!; Site 2: Sall;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
1 (bases 1 to 316)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                       Indels
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100.0%; Score 21; DB 29; 100.0%; Pred. No. 8.4;
                                                       Mismatches
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Xenopus laevis
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/mol_type="mRNA"
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KEYWORDS
SOURCE
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ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/db xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Weator: phOS1; Site:" BSE 1; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S.
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb) : The v + i method used for the library construction is described in Getail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB812595
SWWDmfCAV08B01SK Wuchereria bancrofti microfilaria cDNA
(SAN95SjL-WDMf) Wuchereria bancrofti cDNA clone SWWDmfCAV08B01 5',
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Wuchereria bandrofti
Bukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchoceroidae; Wuchereria.
1 (bases 1 to 73)
Williams, S.A.
                                                                        Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes expressed in microfilaria of Wuchereria bancrofti
Unpublished (1996)
Contact: Seven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.7%; Score 18; DB 28; Length 915; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA 171: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Wuchereria bancrofti"
/mol_type="mRNA"
/db_xref="taxon:6293"
                                                                                                                                                                       High quality sequence start: 176
High quality sequence stop: 283.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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Conservative 0;
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                                                                                                                   DNA library
Seg primer: M13-Reverse
Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 4135853826
Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
CB832595
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Best Local Similarity
Matches 18; Conserv
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CB832595/c
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                    AZ677920 915 bp DNA linear GSS 14-DEC-2000 ENTHK83TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
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Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebiae; Entamoeba.
1 (bases 1 to 915)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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GSS.
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RESULT 5 AZ677920/c DEFINITION

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ORIGIN

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

ACCESSION VERSION KEYWORDS

EST 21-APR-2003

Gaps .. 0

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CK107208 252 bp mRNA linear BST 01-DEC-2003
UB49DPG02.5pR Populus active cambium cDNA library Populus tremula
cDNA clone UB49DFG02 5', mRNA sequence.
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Striky, F., Bhalerao, R.R., Unneberg, P., Segerman, B., Nilsson, P.,
Brunner, A.M., Campaa, L., Jonsson-Lindvall, J., Tandre, K.,
Strauss, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalerao, R.P.,
Nilsson, O., Sandberg, G., Karlsson, J., Lundeberg, J. and Jansson, S.
M. Appulus EST resource for functional genomics
Unpublished (2003)
Other ESTs: UB49DFG02, UB49DFG02.3pR
Contact: Bo Segerman
Umea Plant Science Center, Department of Plant Physiology
                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Malpighiales, Salicaceae, Saliceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Populus tremula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6279
Email: bo. segerman@plantphys.umu.se.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:113636"
/clone="UB49DPG02"
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    68 GIGCCAGCAGCAGCGGI 84
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1 (bases 1 to 413)
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Populus tremula
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AU007074/c
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                                                                                                          Anote—10. Thomaton Uni-ZAP XR; Site_1: Eco RI, Site_2: Xho I; Lymphatic filarial nematode parasite of humans.—RNA was prepared from approximately 85,000 microfilariae isolated from the blood of an infected individual from Guyana, South America and converted to double-stranded conventiage reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library has 2.9 x 1085 independent recombinants and the average insert size is -libr. The library was constructed by Sandra J. Laney. The genome@smith.edu."
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CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Schizosaccharomyces pombe late log phase cDNA"/note="Vector: Ml3mp19; The cDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 148)
Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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AU010207 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc05561, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mitsucki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nis.go.jp.
Location/Qualifiers
                                                                     clone_lib="Wuchereria bancrofti microfilaria cDNA
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Bukaryota, Pungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycet
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                  81.0%; Score 17; DB 14; Length 73; 100.0%; Pred. No. 3.9e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (fission yeast)
                        'dev_stage="microfilaria"
/lab_host="XL1-Blue MRF'"
clone="SWWbmfCAV08B01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4896"
/clone="spc05561"
/sex="h minus"
                                                                                           (SAW95Sjl-WbMf)"
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AU010207.1 GI:3346887
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Best Local Similarity 100.0
Matches 17; Conservative
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Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                       AU007074 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc01418, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
/tissue_type="Active_cambium"
/clone_lib="Populus_active_cambium_cDNA_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                   81.0%; Score 17; DB 14; Length 252; 100.0%; Pred. No. 4.6e+02;
                                                                                                                                                          Indels
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Schizosaccharomyces pombe
                                                                                                                      100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ūnpublished (1998)
Contact: Mitsucki Morimyo
                                                                                                                                                                                                                                                        189 CAGCAGCAGCGCTAATA 205
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AU007074.1 GI:3343532
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GTGCCAGCAGCAGCGGT 17

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Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone
probably contains an inverted insert. The sequence has been trimmed
and the T residues removed.
                                                                                                                                                                                                                                                                                 AA695154 linear EST 23-APR-2001 GM02326.3prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM02326 3prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="GM Drosophila melanogaster ovary BlueScript" /note="Organ: ovary; Vector: BlueScript SK; Site 1: BcoRI; Stte_2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at EcoRI and XhoI in BlueScript SK(+/-)"
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                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 475)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Bropy-HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW940266 524 bp mRNA linear EST 02-DEC-20 GH07623.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH07623 3 similar to CG5514: FBan0005514 GO:[] located on: 3R 98B2-98B2;: 08/12/2002, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="newly eclosed females: germarium-stage 6"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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81.0%; Score 17; DB 12; Length 460; 100.0%; Pred. No. 5e+02; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/mol type="mRNA"
/db_xref="taxon:727"
/clone="GM02326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: 23 row: C column: 2
High quality sequence stop: 406.
Location/Qualifiers
     81.00,
100.0%; Pre-
                                                                                                                                                         156 TGCCAGCAGCAGCGTA 140
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                                                                                                       2 TGCCAGCAGCAGCGGTA 18
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stapleton, M.
                           Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                AA695154
     Query Match
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AW940266/c
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                                                                                                                                                                                                    /clone_libe="Schizosaccharomyces pombe late log phase cDNA" hote="Weetor: Ml3mpl9; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mpl9 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003763: arm:3R [23621985,23825541]
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/sex="male and female"
/dev stage="adutt"
/lab host="DH5 - alpha"
/clone lib="GH Drosophila melanogaster head por2"
/note="Torgan: head, Vector: por2; Site 1: EcoRI; Site 2:
XhoI; Sized fractionate DNAs were directly ligated Into
por2. Plasmid cDNA library."
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Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Brarycota; Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 460)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubhi, G.M.
DEMPSP/HHMI Drosophila EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 413;
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                                   1. .413
'organism="Schizosaccharomyces pombe"
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/organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                          81.0%; Score 17; DB 9; L. 100.0%; Pred. No. 4.9e+02; iive 0; Mismatches 0;
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Plate: GH.63 row. G column: 3
High quality sequence stop: 444.
Location/Qualifiers
                                                                                                                             /db_xref="taxon:4896"
/clone="spc01418"
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/db_xref="taxon:7227"
/clone="GH06375"
  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Other ESTs: GH06375.5prime
Contact: Stapleton, M.
                                                                         /mol_type="mRNA"
/strain="972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG632306.1 GI:13757423
                                                                                                                                                                              /sex="h minus'
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                              source
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BG632306/c
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ORIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (baees 1 to 554)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
more T residues at the beginning of the sequence, this clone probably contains an inverted insert. The resulting Poly-T sequence has been removed.

Plate: 379 row: H column: 12

High quality sequence stop: 440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF331275
RCS-BT0377-030200-012-G03 BT0377 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                             /dev stage="0" to 24 hours mixed stage embryonic"
/lab host="Xil Blue"
/clone lib="iD Drosophila melanogaster embryo pOT2"
/note="Organ: embryo; Vector: pOT2; Site 1: EcoR1; Site 2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-BT0377-030200-012-G03&t3=2000-02-03&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.0%; Score 17; DB 9; Length 540
100.0%; Pred. No. 5.1e+02;
iive 0; Mismatches 0; Indels
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organism="Drosophila melanogaster"
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High quality sequence stop: 91.
Location/Qualifiers
1. 554
//organism=Homo sapiens"
//mol_type="mRNA"
//db zref="taxon:9606"
//dev_stage="Adult"
                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:7227"
/clone="LD37996"
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nes 17; Conserv
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BF331275/c
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                                                                                                                                                                                                                                                                                                                                                 Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Berkeley, CA 94720, USA
Fax: 510 486 6798
Berkeley, carg/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyaden/lated. The resulting Poly-T sequence has been removed. hit
genomic AE003763: Drosophila melanogaster genomic scaffold
14200013386035 section 88 of 105, complete sequence.: 02/16/2001
Plate: GH.76 row: B column: 11
High quality sequence stop: 382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male and female"
/dev stage="adult"
/dev stage="adult"
/lan_host="DHS - alpha"
/clone=ith="GH Drosophila melanogaster head port"
/note="organ: head; Vector: ports; Site 1: EcoRI; Site 2:
Xhol; Sized fractionated cDNAs were directly ligated intoport.
Plasmid cDNA library."
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One Cyclotron Rd, Berkeley, CA 94720, USA
One System 866 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
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Drosophila melanogaster
Drusophila melanogaster
Brusryota; Metazoa; Arthropoda; Hazapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (Dases 1 to 540)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
Broky, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
Broky, M.M. Drosophila EST Project
                                                                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 524)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                 Unpublished (2001)
Other ESTs: GH07623.5prime
Contact: Stapleton, M.
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100.0%; Pre-
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AI518472.1 GI:4424326
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Matches 17; Conservative
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AI518472/c
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Gaps .,

Length 540;

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Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

1 (bases 1 to 619)

Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L.,

Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyee, E.,

Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K.,

Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S.,

Trujillo, R., Valentine, J., Wells, A., Werner Washburne, M., Yazzie, S.

and Natvig, D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev stage="germinating conidia"
/clone_lib="Conidial"
/note="mRNA isolated from germinating conidia, grown in lx Vogel's, 2% sucrose for 4.5 hours. cDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI397756 619 bp mRNA linear EST 08-FEB-1999 NCC5H8T3 Conidial Neurospora crassa cDNA clone NC5H8 5', mRNA
                  /note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed sequences from conidial, mycelial, and sexual stages of Neurospora crassa
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                      81.0%; Score 17; DB 10; Length 554; 100.0%; Pred. No. 5.1e+02; ive 0; Mismatches 0; Indels
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Department of Biology
University of New Mexico
Castetrer Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Neurospora crassa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fungal Genet. Biol. 21, 348-363 (1997)
97435549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="74-OR23-IV A"
/db_xref="taxon:5141"
/clone="NC5H8"
                                                                                                                                                                   stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Mating type A"
/tissue_type="Conidia"
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    Location/Qualifiers
clone lib="BT0377"
                                                                                                                                                                                                                                                                                                                                        3 GCCAGCAGCAGCGGTAA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI397756.1 GI:4240841
EST.
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
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AI397756/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
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MEDLINE
PUBMED
COMMENT
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AUTHORS
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279 GIGCCAGCAGCAGT 263
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Search completed: August Job time : 1466.92 secs

4, 2004, 09:20:58

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1 GTGCCAGCAGCGGT 17

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Gaps

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Query Match

81.0%; Score 17; DB 9; Length 619;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Fusobacterium nucleatum
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16; Conservative
Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1502
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Sequence 5583, Ap
Sequence 5383, Ap
Sequence 531, Ap
Sequence 27485, A
Sequence 12478, A
Sequence 12478, A
Sequence 12478, A
Sequence 12478, A
Sequence 166711,
Sequence 166711,
Sequence 166711,
Sequence 16711,
Sequence 2841, Ap
Sequence 2761, Ap
Sequence 602, App
Sequence 10712, A
Sequence 10712, A
Sequence 20052,
Sequence 10712, A
Sequence 20052, A
Sequence 1032, A
Sequence 10312, A
Sequence 10392, A
                                                       August 4, 2004, 06:43:54; Search time 218.94 Seconds (without alignments) 247.629 Million cell updates/sec
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                                                                                                                                                                                                                                                 Pending Patents_NA_New:*

1. (cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

2. (cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

3. (cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5. (cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5. (cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6. (cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

7. (cgn2_6/ptodata/2/pna/USO0_NEW_COMB.seq:*

8. (cgn2_6/ptodata/2/pna/USO0_NEW_COMB.seq:*

9. (cgn2_6/ptodata/2/pna/USO0_NEW_COMB.seq:*

9. (cgn2_6/ptodata/2/pna/USO0_NEW_COMB.seq:*
                                                                                                                                                                                        9508132
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-729-961-1
US-09-404-520B-583
US-10-896-891-531
US-10-100-683-3306
US-09-248-796A-3573
US-10-767-701-12478
US-09-404-520B-9481
US-09-404-520B-9481
US-09-404-520B-9481
US-09-404-520B-9481
US-10-100-683-13121
US-10-100-683-13121
US-10-100-683-13121
US-10-100-683-13121
US-10-745-414-764
US-10-745-444-764
US-10-745-444-764
US-10-745-444-764
US-10-745-444-764
US-10-100-683-13121
US-10-745-471-10712
US-10-747-471-10712
US-10-744-333A-600711
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                      4754066 segs, 1232178907 residues
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                                          nucleic search, using sw model
                                                                                                                                                                                                                                  Post-processing: Listing first 45 summaries
                                                                                                            1 acaaggcccgagaacgtattca 22
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Gapop_60.0 , Gapext 60.0
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22
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Sequence 36908, A Sequence 213, Ap Sequence 2213, Ap Sequence 2213, Ap Sequence 2447, Ap Sequence 2646, A Sequence 26196, A Sequence 26196, A Sequence 26196, A Sequence 28589, A Sequence 9568, Ap Sequence 9569, Ap Sequence 2882, Ap Sequence 2882, Ap Sequence 2882, Ap Sequence 2643, Ap Sequence 164349, Ap Sequence 164349, Ap
US-09-404-520B-36908

US-60-579-902-11666

US-60-579-902-1233

US-60-579-662-2213

US-10-834-967-2447

US-10-834-967-2447

US-10-834-967-2447

US-09-404-520B-26196

US-09-404-520B-26196

US-09-404-520B-26196

US-10-425-115-108619

US-10-896-891-9569

US-10-896-891-9569
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RESULT 1
US-10-729-961-4/c

Sequence 4, Application US/10729961

APPLICANT: INAON, Varihide

APPLICANT: TIANO, Workhide

TITLE OF INVENTION: Frience For Detecting Fusobacterium Nucleatum By Pcr Methods And

TITLE OF INVENTION: For Detection

TITLE OF INVENTION: For Detection

FILE REPRENCE: 246312USO

CURRENT APPLICATION NUMBER: US/10/729,961

CURRENT FILING DATE: 2003-12-0

PRIOR PILING DATE: 2002-12-10

PRIOR PILING DATE: 2003-12-0

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3:1
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US-10-729-961-1/c
US-10-729-961-1/c
Sequence 1, Application US/10729961
Sequence 1, Application US/10729961
Sequence 1, Application US/10729961
Sequence 1, Application Sequence 1, Application Sequence 1, Application Sequence 1, Application Moribide
APPLICANT: ITANO, Worlhide
TITLE OF INVENTION: Painers For Detecting Fusobacterium Nucleatum By Pcr Methods And
TITLE OF INVENTION: Por Detection
FILE REFERENCE: 246312030
CURRENT APPLICATION NUMBER: US/10/729,961
CURRENT FILING DATE: 2003-12-09
PRIOR FILING DATE: 2002-12-10
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100.0%; Pred. No. 0.47;
ative 0; Mismatches
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Query Match
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; Sequence 531. Application US/10896891
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CANCER, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CLO00788
; CURRENT APPLICATION NUMBER: US/10/896,891
; CURRENT PELLING DATE: 2004-07-23
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 12618
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 531
LENGTH: 281443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Coc., Yongwei
APPLICANT: Hinke, Gregory J.
APPLICANT: Hinke, Gregory J.
APPLICANT: Hinke, Gregory J.
APPLICANT: McIninch, James
APPLICANT: W. Jachyuk
APPLICANT: W. Jachyuk
APPLICANT: Y. Jachyuk
APPLICANT: Short Jaic
TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/404,520B
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
SEQ ID NO 5583
LENGTH: 8004
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                              ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1650)..(1650)
; OTHER INFORMATION: n stands for any base
US-10-729-961-1
PRIOR APPLICATION NUMBER: JP 2003-403715
PRIOR FILING DATE: 2003-12-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1661
TYPE: DNA
ORGANISM: Fusobacterium nucleatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
2.09-404-520B-5583/C
3.Sequence 5583, Application US/09404520B
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1367 CCCGAGAACGTATTCA 1352
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Best Local Similarity 100.
Matches 16; Conservative
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; ORGANISM: Human
US-10-896-891-531
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US-09-404-520B-27485
US-09-404-62 Application US/09404520B
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Timberlake, William E.
APPLICANT: Timberlake, William E.
APPLICANT: Yu, Jaehyu,
APPLICANT: Yu, Jaehyu,
TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
TITLE REFRENCE: 38-10(15498) A
CURRENT APLICATION NUMBER: US/09/404,520B
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
SEQ ID NO 27485
LENGTH: 1080
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NUMBER OF SEQ ID NOS: 13468
SOFTWARE: Patentin Ver. 2.0
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68.2%; Score 15; DB 6; Length 281443; 100.0%; Pred. No. 2.9;
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                                                         0; Indels
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF LINGHILON: HUMBER: US/10/100,683
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR FILING DATE: 1997-03-07
PRIOR PELLING DATE: 1997-04-11
PRIOR PELLING DATE: 1997-04-11
PRIOR PELLING DATE: 1997-04-11
PRIOR PELLING DATE: 1997-04-11
PRIOR PELLING DATE: 1997-06-23
PRIOR PELLING DATE: 1997-06-23
PRIOR PELLING DATE: 1997-06-22
PRIOR PELLING DATE: 1997-06-11
PRIOR PELLING DATE: 1997-06-11
PRIOR PELLING DATE: 1997-04-11
PRIOR PELLING DATE: 1997-04-11
PRIOR PELLING DATE: 1997-04-11
PRIOR PELLING DATE: 1997-04-11
PRIOR PELLING DATE: 1997-06-22
PRIOR PELLING DATE: 1997-06-21
PRIOR PELLING DATE: 1997-06-11
PRIOR PELLING DATE: 1997-06-22
PRIOR PELLING DATE: 1997-06-22
PRIOR PELLING DATE: 1997-06-22
                                                                                                                                                                                                                                                                                                                                                                                      Human Secreted Proteins
                                                                                                                                                                                                                                                                             US-10-100-683-3306; Sequence 3306, Application US/10100683; GENERAL INFORMATION:
           68.20.
100.08; Pre
                                                                                                                                                                  240133 GCCCGAGAACGTATT 240119
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Best Local Similarity 100.
Matches 14; Conservative
                                                            Conservative
                                                                                                                 6 GCCCGAGAACGTATT
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; ORGANISM: Homo sapiens
US-10-100-683-3306
                            Best_Local Similarity
Matches 15; Conserv
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Sequence 166711, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                         APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Timberlake, William E.
APPLICANT: McIninch, James
APPLICANT: W. Jachyuk
APPLICANT: Y. Jachyuk
APPLICANT: McIninch, Jachyuk
APPLICANT: Ghodssi, Azita
TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/404,520B
CURRENT APPLICATION NUMBER: 1999-09-23
SURMENT FILING DATE: 1999-09-23
SEQ ID NOS: 44345
LENGTH: 1379
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, James
APPLICANT: McIninch, James
APPLICANT: W. Jachyuk
APPLICANT: Yu, Jachyuk
APPLICANT: Yu, Jachyuk
APPLICANT: APICANICA: Bareitcella nidulans Genome Sequence and Uses Thereof
FILE REFERENCE: 38-10(15498)A
CURRENT APPLICATION NUMBER: US/09/404,520B
CURRENT APPLICATION NUMBER: US/09/404,520B
NUMBER OF SEQ ID NOS: 44345
SEQ ID NO 20466
LENGTH: 1389
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red. No. 10;
Mismatches 0
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches (
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; Sequence 20466, Application US/09404520B
; GENERAL INFORMATION:
                       US-09-404-520B-9481
; Sequence 9481, Application US/09404520B
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 14; Conservative 0
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ORGANISM: Emericella nidulans
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TITLE OF INVENTION: VOCAETC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: VOCAETC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT PAPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PLING DATE: 1998-02-13
PRIOR PLING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
FRIOR FILING DATE: 1998-08-13
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US-10-76-701-12478

Sequence 12478, Application US/10767701

Sequence 12478, Application US/10767701

Sequence 12478, Application US/10767701

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT PLING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 12478

LENGTH: 1271
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US-10-767-701-12478
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10;
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63.6%; Score 14; DB:
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches
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100.0%; Pre
; TYPE: DNA; ORGANISM: Emericella nidulans
US-09-404-520B-27485
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Best Local Similarity 100.0
Matches 14, Conservative
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Matches
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cao, Yongory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Timberlake, William E.

APPLICANT: Morninch, James

APPLICANT: Worninch, James

APPLICANT: Worninch, Azita

TITLE OF INVENTION: Emericalla nidulans Genome Sequence and Uses Thereof

TITLE REPERENCE: 38-10(15498) A

CURRENT APPLICATION NUMBER: US/09/404,520B

CURRENT FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 44345

SEQ ID NO 14910

LENGTH: 1866
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Pred. No. 11;
0; Mismatches 0; Indels
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Pred. No. 10;
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                                                                                                                                       , OTHER INFORMATION: Clone ID: MRT4577_83619C.1
US-10-425-115-166711
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Sequence 2841, Application US/10100683
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 166711
LENGTH: 1553
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Best Local Similarity
                                                                   TYPE: DNA
ORGANISM: Zea mays
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PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1997-06-802
PRIOR FILING DATE: 1997-06-802
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 13468
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2841
LENGTH: 1959
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Pred. No. 11;
0; Mismatches 0; Indels
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Pred. No. 11;
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APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Gastle, Arthur
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
FILE REFERENCE: 44921-5038-01-WO
CURRENT APPLICATION NUMBER: US/10/501,933
CURRENT FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
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GENERAL INFORMATION:
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100.0%; Pre
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ORGANISM: Homo sapiens
US-10-100-683-2841
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ORGANISM: Homo sapiens
FEATURE:
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PRIOR FILING DATE: 2000-11-02
PRIOR PLICATION NUMBER: US 60/290,029
PRIOR PLIING DATE: 2001-05-11
PRIOR PLIING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR PLIING DATE: 2001-05-15
PRIOR PLIING DATE: 2001-05-25
PRIOR PLIING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR PLIING DATE: 2001-06-13
PRIOR PLIING DATE: 2001-07-09
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CRGANISM: Rattus norvegicus
FEATURE:
COMBANISM: Restus norvegicus
COMBANISM: Restus Norvegicus
COMBANISM:
COMBANION: Genbank Accession No. X83231
US-10-501-933-4270
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Segmence 3. Appli	mience 2	equence 2	ì	e	יי ט	י טור	Ċ,	1, Appl	H	1, 4	e 94,	6	equence 4,	equence 5,	9	Sequence 2, Appli	equence 4.	equence	A donaine	equence 2.	A enterta	odione 5	າ u	education	· •	4, 1	equence 5,	ednence 6,	equence 3,	equence 3, Appl	equence 3,	equence 3, Appl	equence 7,	Sequence 7, Appli	~	Sequence 7, Appli	4	'n	quence 2,	o o	הסתפות	ì	o duration of) (, (adrence
ID	***********	9 US-09-940-860-3	PCT-11801-160304	-03501-	20200	1000	2 - 000 - 000 - 000 - 00 - 001 - 00 - 00	01011010	-0/-923-8/1B-	-07-923-871B-	-07-923-871-	US-07-923-871A-1	US-10-061-071-94	US-09-548-998	US-09-548-	US-09-548-	US-09-548-998A-	US-09-548-998C-	TIS-09-548-998C-	TIS-09-548-998C-	178-09-548-9987-	ITS-09-548-998E-	TC-00-548-998E-	H800-847-80-211	110 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0	1001010101010101	- TO - TO - OIL OIL	US-10-001-071-		US-10-061-071-6		US-09-548-	US-09-548-998E	US-10-061-071-3	US-09-548-	US-09-548-998	US-09-548-998E			US-09-786-253-5	PCT-US98-12764-	US-09-830-228-	- 17598-12764-	115-06-83-07-311	71-080-01-011 0	201-027-01-00 301-027-00-011	101 001 00 011	20 - 438 - TS	US-08-89-50
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ALIGNMENTS

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APPLICANT: MOSIMILA MULIA TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA FILE REFERENCE: 01107.001862 CURRENT APPLICATION NUMBER: US/09/940,860 CURRENT FILING DATE: 2001-08-29 PRIOR APPLICATION NUMBER: 60/229,376 PRIOR PILING DATE: 2000-08-31 NUMBER OF SEQ ID NOS: 7 SOFTWARE FASTSEQ for Windows Version 4.0 SEQ ID NO 3 SEQ ID NO 3 SEQ ID NO 3
Sequence 3, Application US/09940860; GENERAL INFORMATION:
APPLICANT: Rothman, Richard
                                                                                                                                                                                                                                                                                                                                                                                                          . TYPE: DNA ORGANISM: Artificial Sequence
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PAPPLICANT: University of Maryland Biotechnology Institute
APPLICANT: University of Maryland Biotechnology Institute
TITLE OF INVENTION: Stimulation of Microbial Dechlorination of Polychlorinated Biphen
TITLE OF INVENTION: Halogenated Ethenes
TITLE OF INVENTION: Halogenated Ethenes
TITLE OF INVENTION: Halogenated Ethenes
CURRENT APPLICATION NUMBER: PCT/US03/03202
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 60/353,134
PRIOR PELING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 336
TYPE: DNA
ORGANIEM Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Maryland Biotechnology Institute
APPLICANT: Sowers, Kevin R.
APPLICANT: Sowers, Kevin R.
APPLICANT: Sowers, Kevin R.
APPLICANT: Compositions and Methods for Microbial Dechlorination of Polychlo TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of Polychlo TITLE OF INVENTION: Biphenyl Compounds
FILE REFERENCE: 4115-149 PCT
CURRENT FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 2
LENGTHE: 316
LENGTHE: 316
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                                                                                      Length 22;
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Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 22; DB 1; Length 336; Best Local Similarity 100.0%; Pred. No. 0.0076; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                 0; Indels
; OTHER INFORMATION: synthetic amplification primer US-09-940-860-3
                                                                                   Query Match
100.0%; Score 22; DB 39;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

OTHER INFORMATION: Synthetic Construct
PCT-US03-03202-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

, OTHER INFORMATION: Synthetic construct

PCT-US01-16030A-2
                                                                                                                                                                                                                                                                                                                                                   RESULT 2
PCT-USO1-16030A-2/c
Sequence 2, Application PC/TUS0116030A
GENERAL INFORMATION:
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GENERAL INFORMATION:
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PCT-US03-03202-2/c
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Sequence 35, Application US/07923871B
GENERAL INFORMATION:
HORSEAL INFORMATION:
TITLE OF INFORMATION:
METHOD FOR SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY:
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: IBM PC COMPATION:
MEDIUM TYPE: FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/923,871B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 22; DB 3; Length 368; 100.0%; Pred. No. 0.0076;
GENERAL INFORMATION:
APPLICANT: White Ph.D, Thomas J.
APPLICANT: Wise Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,871B
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: PERLY, DOUGLES A:
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8697
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 acaaggcccgagaacgrarrca 252
                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAAGGCCCGAGAACGTATTCA 22
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MOLECULE TYPE: DNA (genomic)
US-07-923-871B-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510) 814-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (510) 814-2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                    Sequence 2, Application PC/TUS0303202A
GENERAL INFORMATION:
GURRENT APPLICATION NUMBER:
GURRENT FILING DATE:
GOS-02-03
PRIOR APPLICATION NUMBER:
GOS-02-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-860-200D-2/c
US-09-860-200D-2/c
J Sequence 2. Application US/09860200D
J GENERAL INFORMATION:
APPLICANT: Kevin, Bowers R.
APPLICANT: Kevin, Bowers R.
TILLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of TILLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of TILLE OF INVENTION: Polychlorinated Biphenyl Compounds
TILLE REFERENCE: 4115-149
CURRENT APPLICATION NUMBER: US/09/860,200D
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/266,650
PRIOR FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 336
LENGTH: 336
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100.0%; Score 22; DB 35; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 22; DB 1; Length 336; Best Local Similarity 100.0%; Pred. No. 0.0076; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Synthetic Construct PCT-US03-03202A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Synthetic Construct US-09-860-200D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 ACAAGGCCCGAGAACGTATTCA 302
                                                   323 ACAAGGCCCGAGAACGTATTCA 302
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US-07-923-871B-36/c
; Sequence 36, Application US/07923871B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                    -US03-03202A-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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Sequence 1, Application US/07923871

Sequence 1, Application US/07923871

APPLICANT: White Ph.D. Thomas J.

TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: N
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER: EAPLABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
ORPHARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/923,871
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 22; DB 3; Length 498; Best Local Similarity 100.0%; Pred. No. 0.0074; Matches 22; Conservative 0; Mismatches 0; Indels
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/ABOTH INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8697
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 014-2863
TELEFRAX: (510) 814-2863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 ACAAGGCCCGAGAACGTATTCA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAAGGCCCGAGAACGIATICA 22
                                                                                                                                                                                                                                                       complement (164..165)
                                                              complement (35..36)
                                                                                                                                                                                                                                                                                                                                                                                  complement (169)
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                                                                                                                                                                                                                                                                                                                      complement (167)
                                                                                                                           complement (41)
                                                                                                                                                                                          complement (67)
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SEQUENCE CHARACTERISTICS:
LENGTH: 505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                        unsure
                                                                                                                                                                                                                                     unsure
                                                                                                                                                                                                                                                                                                    unsure
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                                                                                                           unsure
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                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY:
; LOCATION:
US-07-923-871B-1
                                        NAME/KEY:
LOCATION:
FEATURE:
                                                                                                     NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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FEATURE:
NAME/KEY:
LOCATION:
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Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White Ph.D, Thomas J.
APPLICANT: Odge, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NJ
COUNTRY: USA
ZUP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: FlOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,871B
CLASSIFICATION: 435
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8697
TELEPHONE: (510) 814-2974
TELEPHONE: (510) 814-2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLAUSE TECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A:
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8697
TELEPHONE: (510) 814-2974
TELEPHONE: (510) 814-2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 ACAAGGCCCGAGAACGTATTCA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 498 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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US-07-923-871B-1/c
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Sequence 94, Application US/10061071
Sequence 94, Application US/10061071
Sequence 97, Application US/10061071
APPLICANT: B.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HINDRICKSON, EDWIN
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: BC1002 US CIP
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/129,511
PRIOR APPLICATION NUMBER: G0/129,511
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
SEQ ID NO 94
LENGTH: 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ebersole, Richard C.
APPLICANT: Ebersole, Richard C.
APPLICANT: Ebersole, Edwin
TITLE OF INVENTION: DUCLETC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
FILE REPERBRÜCE: BCI002 US NA
CURRENT APPLICATION NUMBER: US(09/548,998A
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 22; DB 3; Length 50; Pred. No. 0.0074; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Dehalococcoides related Family A Group US-10-061-071-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1004 ACAAGGCCCGAGAACGIATICA 983
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; Sequence 2, Application US/09548998A
; GENERAL INFORMATION:
                                                                        complement (35..36)
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Best Local Similarity 100.0%;
Matches 22; Conservative 0;
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Best Local Similarity 100.0%;
Matches 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                            complement (167)
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complement (169)
                                                                                                                                                                                                                                (67)
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complement
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FEATURE:
NAME/KEY:
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FEATURE:
ANTI-SENSE:
FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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; LOCATION:
US-07-923-871A-1
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APPLICANT: White Ph.D. Thomas J.
APPLICANT: Dodge, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCE: 30
CORRESPONDENCE ADDRESS:
ADDRESSES: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STARE: NJ
COUNTY: USA
ZIP: O7110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BATCATION DATA:
APPLICATION NUMBER: US/07/923,871A
FILING DATE:
CLASSIFICATION NUMBER: US/07/923,871A
FILING DATE: OF-MAR-1990
ATPORTY NOT-MAR-1990
ATPORTY NUMBER: 32,630
REGISTRATION TOPMARTION:
NAME: Sias, Stace R.
TELECOMUNICATION INPERE: 32,630
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 22; DB 3; Length 505; Best Local Similarity 100.0%; Pred. No. 0.0074; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 ACAAGGCCCGAGAACGTATTCA 375
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                                                                                                                                                                                                                                                                                                                    complement (164..165)
                                                                                complement (35..36)
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3: DNA (genomic)
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complement (169)
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
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LOCATION:
FEATURE:
  ANTI-SENSE:
FEATURE:
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, LOCATION:
US-07-923-871-1
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Search completed: August
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APPLICANT: Bersola.
APPLICANT: Bersola.
TITLE OF INVENTION:
TITLE OF INVENTION WICHERLA
TITLE OF INVENTION WICHERLA
TITLE OF INVENTION WICHERLA
CURRENT APPLICATION NUMBER: US/09/548,998A
CURRENT APPLICATION NUMBER: 60/129,511
PRIOR PELICATION NUMBER: 60/129,511
PRIOR PELICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09548998A
Sequence 5, Application US/09548998A
Sequence 5, Application US/09548998A
Sequence 5, Application Security Sequence 5, Application Sequence 5, TITLE OF INVENTION: BACTERIA APPLICATION BACTERIA FILE OF INVENTION: BACTERIA SEQUENCE: BOLIOG 208 NA
FILE REPRENDENCE: BOLIOG 208 NA
CURRENT PILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 60
SSO ID NOS: 60
SSO ID NO 5
IENGTH: 1377
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100.0%; Score 22; DB 23; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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100.0%; Score 22; DB 23; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                      0; Indels
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100.0%; Score 22, DB 23;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 22; Conservative 0; Mismatches 0;
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                                                                                                                                                       TYPE: DNA
ORGANISM: Dehalococcoides ethenogenes
                                                                                                                                                                                                                                                                                                                                                                                                                       1321 ACAAGGCCCGAGAACGTATTCA 1300
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; ORGANISM: Dehalococcoides ethenogenes
US-09-548-998A-5
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
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US-09-548-998A-4/c
                                                                                                                                    LENGTH: 1377
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APPLICANT: Ebersole, Richard C.
APPLICANT: Ebersole, Richard C.
APPLICANT: Bensole, Richard C.
APPLICANT: Bensole, Richard C.
APPLICANT: Hendrickson, Edwin
TITLE OF INVENTION: BACTERIA
FILLE OF INVENTION: BACTERIA
FILLS OF INVENTION: 00-10
FRICH APPLICATION NUMBER: US/09/548,998A
CURRENT FILLING DATE: 1999-04-15
NUMBER: OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
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1321 ACAAGGCCCGAGAACGTATTCA 1300
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                                                                         RESULT 15
US-09-548-998A-6/c
; Sequence 6, Application US/09548998A
; GENERAL INFORMATION:
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Matches 22; Conservative
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FEATURE:
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Sequence 94, Appli
Sequence 94, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
                                                                                                                                   August 4, 2004, 07:44:29 ; Search time 199.06 Seconds (without alignments) 541.892 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-61-071-94
US-10-061-071-94
US-10-061-071-4
US-10-061-071-5
US-10-061-071-5
US-10-061-071-5
US-10-061-071-7
US-10-289-762-1
US-10-391-249-16
US-10-391-249-17
US-10-391-249-18
US-10-391-249-18
US-10-391-249-18
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US-10-391-249-18
US-10-391-249-18
US-10-053-078-1
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                                                                                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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22
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Perfect score:
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Sequence 95, Appli
Sequence 1, Appli
Sequence 644, Appli
Sequence 244, Appli
Sequence 229, Appli
Sequence 229, Appli
Sequence 2672, Appli
Sequence 2672, Appli
Sequence 277, Appli
Sequence 277, Appli
Sequence 118, Appli
Sequence 3050, Appli
Sequence 3050, Appli
Sequence 370, Appli
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Sequence 370, Appli
Sequence 379, Appli
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Subjection No. US200400555A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rothman, Richard
APPLICANT: Majundar, Maulik
TITLE OF INVENTION: NOLECTLAR DIAGNOSIS OF BACTEREMIA
FILE REFERENCE: 01107.00185
CURRENT EPLING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
5 US-10-053-078-2

5 US-10-061-071-95

0 US-09-847-513A-1

3 US-10-205-220-1

4 US-10-087-192-544

4 US-10-087-192-544

4 US-10-087-192-544

4 US-10-09-192-544

4 US-10-09-192-54

6 US-10-393-840-239

6 US-09-918-995-32220

0 US-09-918-995-3220

0 US-09-918-995-3220

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0 US-09-918-995-3220

0 US-09-918-995-320

0 US-09-918-995-320

0 US-09-918-910

0 US-09-164-877-40891

0 US-09-164-877-3999

10 US-09-164-877-3999

11 US-10-212-515-3999

12 US-10-212-515-3999

13 US-10-112-1255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: synthetic amplification primer US-09-940-860-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Best Local Similarity 100.
Matches 22; Conservative
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RESULT 2
US-09-860-200D-2/c
) Sequence 2, Application US/09860200D
; Publication No. US20030134408A1
; GENERAL INFORMATION:

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Query Match 100.0%; Score 22; DB 15; Best Local Similarity 100.0%; Pred. No. 0.00045; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 22; DB 15; 100.0%; Pred. No. 0.00045;
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ORGANISM: Dehalococcoides ethenogenes strain DAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
P. ORGANISM: Dehalococcoides ethenogenes strain PL
US-10-061-071-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
    CURRENT APPLICATION NUMBER: US/10/061,071
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/129,511
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION WUMBER: 60/129,511
PRIOR PILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 103
SOFTWARE: MICROSOFT Office 97
SOFTWARE: MICROSOFT Office 97
LENGTH: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1321 ACAAGGCCCGAGAACGTATTCA 1300
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Matches 22, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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| Sequence 94, Application US/10061071 |
| Sequence 94, Application US/10061071 |
| Sequence 94, Application No. US20030077601A1 |
| Publication No. US20030077601A1 |
| Publication No. US20030077601A1 |
| APPLICANT: B.I. DUPONT DE NEMOURS & COMPANY |
| APPLICANT: HENDRICKSON, EDMIN |
| TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING |
| TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING |
| TITLE OF INVENTION: USA CIP |
| TITLE OF INVENTION: USA CIP |
| TITLE OF INVENTION NUMBER: US CIP-29 |
| PRIOR FILING DATE: 1999-04-15 |
| PRIOR PLLING DATE: 1999-04-15 |
| NUMBER OF SEQ ID NOS: 103 |
| SOFTWARRE: Microsoft Office 97 |
| SEQ ID NO 944 |
| SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HENDRICKSON, EDWIN
, *ITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
APPLICANT: Kevin, Bowers R.

APPLICANT: Harold, May D.

TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of TITLE OF INVENTION: Polychlorinated Biphenyl Compounds
FILE REFERENCE: 4115-149
FILE REFERENCE: 4115-149
FILE REFERENCE: 4115-149
FRIOR FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.2
LENGTHARE: PatentIn version 3.2
LENGTHARE: 336
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100.0%; Score 22; DB 10; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 22; Conservative 0; Mismatches 0; Indels
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100.0%; Score 22; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
, ORGANISM: Dehalococcoides related Family A Group
US-10-061-071-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Synthetic Construct US-09-860-200D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 ACAAGGCCCGAGAACGTATTCA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: BC1002 US CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-061-071-2/c
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Sequence 4, Application US/10061071

Sequence 4, Application US/10061071

Publication No. US20030077601A1

GENERAL INPORMATION:
TITLE OF INVERTION: BACTER ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVERTION: MAGNER: US/10/061,071

CURRENT FILING DATE: 2002-01-29

PRIOR APPLICATION NUMBER: US/86/129,511

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Microsoft Office 97

LENGTH: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: NUCLEIC ACID
FILE REFERENCE: BC1002 US CIP
CURRENT APPLICATION NUMBER: US 10/061,071
CURRENT FILING DATE: 2002-01-29
FRIOR FILING DATE: 1999-04-15
FRIOR PLILING DATE: 1999-04-15
FRIOR APPLICATION NUMBER: 06/129,511
FRIOR RILING DATE: 1999-04-15
FRIOR FILING DATE: 1999-04-15
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Length 1377;
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US-LOUGHLY APPLICATION US/10061071
; Sequence 7, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
APPLICANT: B.I. DUPONT DE NEWOURS & COMPANY
APPLICANT: HENDRICKSON, EDWIN
; TITLE OF INVENTION: UGCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
; TITLE OF INVENTION: BACTERIA
; TITLE OF INVENTION: UMBER: US/10/061,071
; CURRENT PELING DAFE: 2002-01-29
; FRIOR APPLICATION NUMBER: US 60/129,511
; PRIOR RILING DATE: 1999-04-15
; PRIOR FILING DATE: 1999-04-15
; NUMBER: OF SEQ ID NOS: 103
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-289-762-1/c
US-10-289-762-1/c
Sequence 1, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Griffals, R.
APPLICANT: GRIFFALS: GRIFFALS: Griffals, R.
APPLICANT: GRIFFALS: G
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Length 1378;
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ilarity 100.0%; Pred. No. 0.00045;
Conservative 0; Mismatches 0;
; Score 22; DB 15;
; Pred. No. 0.00045;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Dehalococcoides ethenogenes strain 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1329 ACAAGGCCCGAGAACGTATTCA 1308
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LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g or
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1). (15000)
OTHER INFORMATION: n=a or c or g or
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      Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (1353)..(1353)
OTHER INFORMATION: N= unknown
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Matches 22, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1443
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Sequence 3, Application US/10061071

Sequence 3, Application US/10061071

GENERAL INFORMATION:

APPLICANT: HENDRATION:

APPLICANT: HENDRATICNS:

APPLICANT: HENDRATICNS:

APPLICANT: HENDRATICNS:

APPLICANT: HENDRATICNS:

APPLICANT: HENDRATICNS:

ATILE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING

TITLE OF INVENTION: BACTERIA

FILE REFERENCE: BC1002 US CIP

CURRENT FILING DATE: 2002-01-29

PRIOR FILING DATE: 1999-04-15

PRIOR PLILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Microsoft Office 97

LENGTH: 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence (A. Application US/10061071)

Sequence (A. Application US/10061071)

Publication No. US20030077601A1

GENERAL INFORMATION:

APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY

APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY

TITLE OF INVENTION: BUTION BUTION

TITLE OF INVENTION: BUTION BUTION

TITLE OF INVENTION: BUTION UNMER: US/10/061,071

CURRENT APPLICATION NUMBER: US/10/061,071

CURRENT APPLICATION NUMBER: US 60/129,511

PRIOR PILING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Microsoft Office 97

LENGTH: 1377
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; OGGANISM: Dehalococcoides ethenogenes strain V/SFD
(S-10-061-071-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 15;
Pred. No. 0.00045;
; Mismatches 0;
                                                                                                                                                                                                                                         Query Match
100.0%; Score 22; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                     ; TYPE: DNA; ORGANISM: Dehalococcoides ethenogenes strain PIN US-10-061-071-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Dehalococcoides ethenogenes strain DLL
US-10-061-071-6
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ilarity 100.0%;
Conservative 0
                 SOFTWARE: Microsoft Office
SEQ ID NO 5
LENGTH: 1377
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Best Local Similarity
Matches 22; Conserval
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NAME/KEY: misc_feature

OTHER INFORMATION: n=a or c or g or

FEATURE: NAME/KEY: misc_feature LOCATION: (12001)..(135000) OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature LOCATION: (105001)..(120000) OTHER INFORMATION: n=a or c or g or '

WANTE KEY: misc feature COCATION: (135001)..(150000)

THER INFORMATION: n=a or c or g or t

'AME/KEY: misc feature COCATION: (150001)..(165000) OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature LOCATION: (165001)..(180000) JTHER INFORMATION: n=a or c or g or

WAME/KEY: misc feature OCATION: (180001)..(195000) THER INFORMATION: n=a or c or g or

NAME/KEY: misc feature LOCATION: (210001)..(225000) THER INFORMATION: n=a or c or g or

WANT/KEY: misc feature LOCATION: (22501)..(24000) THER INFORMATION: n=a or c or

NAME/KEY: misc_feature LOCATION: (19501)..(210000) THER INFORMATION: n=a or c or g or FRATURE:

NAME/KEY: misc feature OCATION: (240001)..(255000) THER INFORMATION: n=a or c or g or t

FEATURE:
NAME/KEY: misc_feature
LOCATION: (255001)..(270000)
OTHER_INFORMATION: n=a or c or g

NAME/KEY: misc feature LOCATION: (270001)..(285000) OTHER INFORMATION: n=a or c

NAME/KEY: misc feature LOCATION: (28501)..(300000) OTHER INFORMATION: n=a or c or g or t

FEATURE: NAME/KEY: misc_feature LOCATION: (300001)..(315000)

NAME/KEY: misc feature LOCATION: (90001)..(105000) JTHER INFORMATION: n=a or c or g or t

FEATURE:
NAME/KEY: misc_feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or

FEATURE:
NAME/KEY: misc_feature
LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g or

NAME/KEY: misc feature LOCATION: (45001)..(60000) OTHER INFORMATION: n=a or c or g or

LOCATION: (30001)..(45000) OTHER INFORMATION: n=a or c or g or

FEATURE:
NAME/KEY: misc_feature
LOCATION: (315001)..(330000)
OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (570001)..(585000) OTHER INFORMATION: n=a or c or g or

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Publication No. US20020192672A1

GENERAL INFORMATION

APPLICANT: Dawson, Jacqueline E.

APPLICANT: Dawson, Jacqueline E.

TITLE OF INVENTION: Jectification of a New Ehrlichia

TITLE OF INVENTION: Species from a Patient Suffering From Ehrlichiasis

TITLE OF INVENTION: Species from a Patient Suffering From Ehrlichiosis

CURRENT APPLICATION NUMBER: US/10/053,078

CURRENT PELLICATION NUMBER: US. 09/061770

PRIOR FILING DATE: 1998-04-16

PRIOR PRILING DATE: 1998-04-16

PRIOR APPLICATION NUMBER: U.S. 07/687,526

PRIOR APPLICATION NUMBER: U.S. 08/147,891
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0
APPLICANT: DOXESY, Stephen J.
TITLE OF INVENTION: CAUSATING OF MYCOPLASMA HYORHINIS AS
TITLE OF INVENTION: CAUSATIVE AGENT FOR SYSTEMIC SCLEROSIS
TITLE OF INVENTION: CAUSATIVE AGENT FOR SYSTEMIC SCLEROSIS
FILE REFERENCE: 07917-142001
CURRENT APPLICATION NUMBER: US/10/391,249
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US 60/364,801
PRIOR FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JANACH LINGALTING SEPHEN J.

TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS TITLE OF INVENTION: CAUGATIVE AGENT FOR SYSTEMIC SCLEROSIS FILE REFERENCE: 07917-142001 CURRENT PILLING DATE: 2003-03-17 PRIOR APPLICATION NUMBER: US 60/364,801 PRIOR PILLING DATE: 2002-03-15 NUMBER OF SEQ ID NOS: 43 SOFTWARE: PSELSEQ for Windows Version 4.0 SEQ ID NO 18 LENGTH: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/10391249; Publication No. US20040091935A1; GENERAL INFORMATION:
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                     72.7%; Sco.
100.0%; Pre
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Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                       TYPE: DNA
COGANISM: Mus musculus
US-10-391-249-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Sus scrofa
US-10-391-249-18
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US-10-053-078-1/c
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US-10-391-249-16/C
| Sequence 16, Application US/10391249
| Sequence 16, Application US/10391249
| Publication No. US20040091935A1
| GREERAL INFORMATION:
| APPLICANT: DOXSEY, Stephen J.
| TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS |
| TITLE OF INVENTION: CAUGATIVE AGENT FOR SYSTEMIC SCLEROSIS |
| FILE REFERENCE: 07917-142001 |
| CURRENT FILING DATE: 2003-03-17 |
| PRIOR APPLICATION NUMBER: US 60/364,801 |
| PRIOR SEQ ID NOS: 43 |
| SEQ ID NO 16 |
| SEQ ID NO 16 |
| LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.7%; Score 16; DB 17; Length 244; 100.0%; Pred. No. 2.8;
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Pred. No. 0.00033;
; Mismatches 0;
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LOCATION: (67501)..(690000)
OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or
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100.08; Pr
                 NAME/KEY: misc feature
LOCATION: (585001)..(600000)
OTHER INFORMATION: n=a or c or g
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                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or
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NAME/KEY: misc feature
LOCATION: (64501)..(660000)
OTHER INFORMATION: n=a or c or
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Best Local Similarity 100.0%;
Matches 22; Conservative 0
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LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c
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LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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Sequence 17, Application US/10391249 Publication No. US20040091935A1

RESULT 12 US-10-391-249-17/c

8 d

US-10-391-249-16 TYPE: DNA

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| FRIOR FILING DATE: 1993-11.05
| FRIOR FILING DATE: 1993-11.05
| FRIOR FILING DATE: 1993-11.05
| FRIOR FILING DATE: 1995-12.02.70
| FRIOR FILING DATE: 1995-10.03
| FRIOR FILING DATE: 10.03
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Search completed: August 4, 2004, 11:56:26 Job time : 201.06 secs

579 CCCGAGAACGTATTCA 564

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August 4, 2004, 04:00:30 ; Search time 180.771 Seconds (without alignments) 517.009 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd..
                                                                                                                                                                                                                                                                                                                    3373863 segs, 2124099041 residues
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                                                                         - nucleic search, using sw model
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22
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Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Word size :

Post-processing: Listing first 45 summaries

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genesequ1990s:* genesequ2000s:* genesequ2001as:* N_Geneseq_29Jan04:* . geneseqn1980s:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2001bs:* geneseqn2004s:* geneseqn2003as:* geneseqn2002s:* 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	uoı	16S ribos	16S ribos	Dehalococ	Intergeni	Intergeni	Intergeni	Intergeni	Intergeni	A 16S rDN	Dehalococ	Dehalococ	Dehalococ	Dehalococ	Dehalococ	A 16S rDN	Dehalococ	Bacterial	Bacterial	Rickettsi	Borrelia	tion (5 of	_	Borrelia
	Description	Aad37948	Aad58507	Aad58049	Aah28398	Aah28396	Aah28401	Aah28397	Aah28399	Aac62240	Aad57959	Aad57957	Aad57961	Aad57960	Aad57958	Aac62244	Aad57962	Aaf31090	Aaf31089	Abs71617	Abs71618	Continuation	Continuation	Aax20249
	. QI	AAD37948	AAD58507	AAD58049	AAH28398	AAH28396	AAH28401	AAH28397	AAH28399	AAC62240	AAD57959	AAD57957	AAD57961	AAD57960	AAD57958	AAC62244	AAD57962	AAF31090	AAF31089	ABS71617	ABS71618	AAX20248 04	AAX91990_10	AAX20249
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	Length	336	336	1014	1284	1284	1284	1284	1284	1335	1377	1377	1377	1377	1378	1443	1443	1451	1451	1479	1515	110000	110000	116277
dю	Query Match	100.00	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	22	22	22	22	. 22	22	22	22	22	22	22	22	22	22	22	22	22	22	. 22	22	22	22	22
	ult No.	: :	N	m	4	2	φ	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23
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4 11		~	Aaq36490 Mycoplasm	ın		Aaq21035 Region sp	٠.	m	Aav43697 Ehrlichia	M			Acd26697 Ehrlichia	Abx93090 DNA seque		P36		Aad58050 Dehalococ	Abz79794 Mycoplasm	1792	Abz79793 Mycoplasm	
AAQ36494	AAQ36491	AAQ36493	AAQ36490	AAQ36495	AAQ21032	AAQ21035	AAQ21034	AAQ15188	AAV43697	ADA18591	ADA18587	ACD26696	ACD26697	ABX93090	ABX93091	AAX61135	AAX61134	AAD58050	ABZ79794	ABZ79792	ABZ79793	
N	N	7	N	N	7	7	7	7	~	ω	Φ	œ	Φ	α	α	N	N	œ	۲-	7	7	
180	187	188	189	191	400	444	539	683	683	683	683	683	683	683	683	938	938	1385	1438	1445	1445	
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72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	
16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	
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J	J	J		J	J	,	J	J			J			J	•	,	•	•	•	•	•	

ALIGNMENTS

RESULT 1

Bioremediative microorganism; 16S ribosomal subunit; dechlorination; PCB; polychlorinated biphenyl; biodegradation; halogenated organic waste; contaminated soil; leachate; aqueous surfactant solution; ds. (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST. AAD37948/c ID AAD37948 standard; DNA; 336 BP. 18-MAY-2001; 2001WO-US016030. 19-MAY-2000; 2000US-0205818P. 06-FEB-2001; 2001US-0266650P. 16S ribosomal DNA (rDNA) #2. (first entry) WPI; 2002-114266/15. May HD; WO200189729-A2. Unidentified. 10-SEP-2002 29-NOV-2001. Sowers KR, AAD37948;

Bioremediative microorganism for dechlorinating chlorinated biphenyls and for bioremediation, comprises a specific 168 ribosomal subunit nucleic for bioremedia acid sequence.

Claim 1; Fig 22; 102pp; English.

The present invention relates to bioremediative microorganisms comprising 16S ribosomal subunit nucleic acid sequence. The microorganisms of the invention are useful for dechlorinating polychlorinated biphenyls (PCBs) including anaerobic dechlorination of ortho- and double-flanked chloro substituents of PCBs. They are useful for biodegradation of halogenated organic waste, e.g., contaminated soil from landfill sites and river beds containing PCBs and to treat leachates and aqueous surfactant solutions resulting from washing the organic waste to transfer PCBs to the aqueous surfactant solutions. The method of the invention is useful for

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The invention relates to an isolated 16S rDNA sequence indicative of a dechlorinating bacterial organism. The invention is useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in various samples. The method of the invention is useful for identifying a dechlorinating bacterial organism that is a member of a cell population or consortium. The isolated bacterial organism is useful for dechlorinating chlorinated compounds which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involves contacting a chlorinated compound with the organism. Oligomuclectide polymer of the invention is useful for separating subfamilies of dechlorinating bacterial organism. The present sequence is Dehalococcoides related family A 165 DHFA sequence
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Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1014 BP; 256 A; 238 C; 309 G; 211 T; 0 U; 0 Other;
                                                                                                                          Dehalococcoides related family A 16S DHFA sequence.
                                                                                                                                                                                     16S rDNA; dechlorinating bacterial organism; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 99-100; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2002; 2002WO-US003927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hendrickson E;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-636804/60.
                                                                                                                                                                                                                                                                                                      WO2003064695-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                various samples.
                                                                                                                                                                                                                                              Unidentified
                                                                 20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ebersole R,
                                                                                                                                                                                                                                                                                                                                                            07-AUG-2003
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17-SEP-2001
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determining the bioremediative potential of CB-containing site, which is useful for monitoring CB-containing site. The invention also relates to compositions which are useful for bioremediation. The present sequence is a 16S ribosomal DNA (rDNA) of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to compositions and methods for bioremediation of polychlorinated biphenyls (PCBs) using dechlorinating microorganisms grown in the presence of stimulating halogenated hydrocarbons and polyhalogenates. Polyhalogenated ethenes are used to stimulate the growth and dechlorinating activity of PCB dechlorinating bacteria in a contaminated soil or sediment. The present
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stimulation of polychlorinated biphenyl dechlorinating bacteria contacting polychlorinated biphenyl dechlorinating bacteria with stimulant having polyhalogenated ethene(s).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polychlorinated biphenyls; PCBs; dechlorinating activity; ds.
                                                                                                                                                                                                        Query Match 100.0%; Score 22; DB 6; Length 336; Best Local Similarity 100.0%; Pred. No. 0.00072; Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                   Sequence 336 BP; 76 A; 83 C; 97 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 336 BP; 76 A; 83 C; 97 G; 80 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                               323 ACAAGGCCCGAGAACGTATTCA 302
                                                                                                                                                                                                                                                                                                                            1 ACAAGGCCCGAGAACGTATTCA 22
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ID AAD58507/C
XX
AC AAD58507;
XX
AAD58507;
XX
AAD58507;
XX
O4-DEC-2003 (first entry)
XX
SW
O64-DEC-2003 (first entry)
XX
W
O7-AUG-2003.
XX
W
W02003065011-A2.
XX
W
W02003065011-A2.
XX
W
W17-AUG-2003.
XX
W
W17-BB-2002; 2003W0-US003202.
XX
W
W17-AUG-2003.
XX
W
W17-2003-638818/60.
XX
XX
W17-BB-2002; 2002US-0353134P.
XX
W17-2003-636818/60.
XX
CUTMA-) UNIV MARYLAND BIOTECHN
XX
CONTACTING POLYCHIORINGED DIP
PT STIMULATION OF POLYCHIORINGED DIP
PT STIMULATION OF POLYCHIORINGED DIP
PT STIMULATION OF POLYCHIORINGED DIP
CC MICTOORGANISMS Grown in the proceed to stimulate the growth a cut of second to second 
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AAD58049/c
ID AAD58
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
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Intergenic spacer; Chlamydiaceae; 168 rRNA; 238 rRNA; Region A; Region B; chlamydial infection; ss.
                                                                                                                                                                          Intergenic spacer between 168 and 23S rRNA genes of strain FML-12.
                                                                                                                                                                                                                                                           Location/Qualifiers
1. .537
/*tag= b
/note= "Region A"
                      1004 ACAAGGCCCGAGAACGTATTCA 983
1 ACAAGGCCCGAGAACGTATTCA 22
                                                                       AAH28398/c
ID AAH28398 standard; rRNA; 1284 BP.
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Gaps

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New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of
                                                                                                                                                                                                                                                     '*tag= d
'note= "Domain I of 23S rRNA"
                                                                                                                                                                     /*tag= c
/note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Col 113-116; 89pp; English.
                                                    Location/Qualifiers
                                                                        /*tag= b
/note= "Region A"
                                                                                                                        /*tag= a
/note= "168 rRNA"
                                                                                                                                                                                                             /*tag= e
/note= "23S rRNA"
                                                                                                                                                                                                                                                                                                        /note= "Region B"
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                                                                                                                                                                                                                                                                          .1086
                                                                                                                                                                                           .1284
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                                                                                                                                                    .444
                            Chlamydophila pneumoniae.
 chlamydial infection; ss.
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                                                                                                                                                                                              445.
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                                                                                                                                                                                                                                                                                                                                       US6261769-B1.
                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                  17-JUL-2001.
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                                                                     misc RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from Chlamydiaceae. The sequences comprise the intergenic spacer between the 16S and the 23S rRNA genes, including the far downstream end of the 16S and the far upstream end of the 23S and the far upstream end of the 23S and the far upstream end of the 23S and 13D region in the 3T end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are probes can be used to identifying and detecting Chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, or to distinguish one strain from another, and for diagnosing chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH28371-AAH28413 represent intergenic spacer target sequences, derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of
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Pred. No. 0.00069;
; Mismatches 0;
                                                                                                                                                       23S rRNA'
                                                            /*tag= c
/note= "intergenic spacer"
445. .1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 119-120; 89pp; English.
                                                                                                                                           /*tag= d
/note= "Domain I of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAAGGCCCGAGAACGTATTCA 46
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                                                                                                /*tag= e
/note= "23S rRNA"
445. .1063
                                                                                                                                                                                            /note= "Region B"
    1. .221
/*tag= a
/note= "168 rRNA"
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AAH28396 standard; rRNA; 1284 BP.
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100.0%;
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                                            .444
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                                                                                                                                                                                                                                                                                                                                          OF AGRIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                          (USDA ) US SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydiaceae.
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                                            misc_RNA
                                                                                                                                                                        misc RNA
                                                                                                                              rRNA
    rRNA
                                                                                      rRNA
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AAH28371-AAH28413 represent intergenic spacer target sequences, derived from Chlamydiaceae. The sequences comprise the intergenic spacer between the 16S and the 23S rRNA genes, including the far downstream end of the 16S and the far upstream end of the 23S domain I flanking intergenic spacer (referred to as Region A), and secondarily, a 131 bp region in the 3' end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are useful for identifying and detecting Chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, on to distinguish one strain from another, and for diagnosing chlamydia! infections in humans and animals. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 22; DB 4; Length 1284; 100.0%; Pred. No. 0.00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1284 BP; 394 A; 218 C; 329 G; 343 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH28401/c
ID AAH28401 standard; rRNA; 1284 BP.
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACAAGGCCCGAGAACGTATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Conservative
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Intergenic spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;

Intergenic spacer between 16S and 23S rRNA genes of strain CWL-029.

RESULT

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AAH28371-AAH28413 represent intergenic spacer target sequences, derived from Chlamydiaceae. The sequences comprise the intergenic spacer between the 16S and the 23S FWA genes, including the far downstream end of the 16S and the far upstream end of the 23S domain I flanking intergenic spacer (referred to as Region A), and secondarily, a 131 bp region in the 3' end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are useful for identifying and detecting Chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, or to distinguish one strain from another, and for diagnosing chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
                                                                                            spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
infection; ss.
                                                                 Intergenic spacer between 168 and 238 rRNA genes of strain TW-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     /*tag= d
/note= "Domain I of 23S rRNA"
959. .1086
/rtag= f
/note= "Region B"
                                                                                                                                                                                                                                                                     /*tag= c
/note= "intergenic spacer"
445. .1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Col 125-128; 89pp; English.
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                /*tag= a
/note= "16S rRNA"
                                                                                                                                                                                                                                                                                                              /*tag= e
/note= "23S rRNA"
145, .1063
                                                                                                                                                                                                      'note= "Region A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00052333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00052333
                           (revised)
(first entry)
                                                                                                                                                                             1. .537
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andersen AA;
                                                                                                                                                                                                                                                          444
                                                                                                                                   Chlamydophila pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USDA ) US SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-440857/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydiaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Everett KDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                       US6261769-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1998;
                          11-SEP-2003
17-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-2001,
                                                                                            Intergenic
chlamydial
                                                                                                                                                                            misc_RNA
                                                                                                                                                                                                                                                           misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                   misc_RNA
                                                                                                                                                                                                                                                                                                  rRNA
                                                                                                                                                                                                                    rRNA
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AAH28171-AAH28413 represent intergenic spacer target sequences, derived from Chlamydiaceae. The sequences comprise the intergenic spacer between the 165 and the 235 rRNA genes, including the far downstream end of the 165 and the far upstream end of the 235 domain I flanking intergenic spacer (referred to as Region A), and secondarily, a 131 bp region in the 3' end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are useful for identifying and detecting Chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, or to distinguish one strain from another, and for disaposing chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                  Intergenic spacer, Chlamydiaceae, 16S rRNA, 23S rRNA, Region A, Region B, chlamydial infection; ss.
                                                                                                                                                                         Intergenic spacer between 16S and 23S rRNA genes of strain CWL-1011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of Chlamydiaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                               *tag= c
note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 115-118; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= d
/note= "Domain I of
                                                                                                                                                                                                                                                                   Location/Qualifiers
67 ACAAGGCCCGAGAACGTATTCA 46
                                                                                                                                                                                                                                                                                           /*tag= b
/note= "Region A"
                                                                                                                                                                                                                                                                                                                                    *tag= a
note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= e
note= "23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Region B"
                                                                                BP.
                                                                                AAH28397 standard; rRNA; 1284
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/*tag= f
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    45. .1284
                                                                                                                                                                                                                                                                                                                                                                                                                                             .1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersen AA;
                                                                                                                                                                                                                                                                                                                                                               . 444
                                                                                                                                                                                                                                         Chlamydophila pneumoniae.
                                                                                                                                                                                                                                                                                  . .537
*tag=
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                                                                                                                                   11-SEP-2003
17-SEP-2001
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                                                                                                         AAH28397;
                                                                                                                                                                                                                                                                               misc_RNA
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                                                                   AAH28397/c
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                                                                                                                                                                                                                                                                                                                                                                                                     rRNA
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                                                     RESULT 7
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Query Match
Best Local Similarity 100.
Matches 22; Conservative

Best Loc Matches

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Gaps

0,

0; Indels

0; Mismatches

100.0%; Score 22; DB 4; Length 1284; 100.0%; Pred. No. 0.00069;

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1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                           Ebersole RC;
                                                                                                                                                                                                                                                                                                                                         13-APR-2000; 2000WO-US009883
                                                                                                                                                                                                                                                                                        Dehalococcoides ethenogenes
                                                                                                                                                                                                                      19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-024581/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 22; Conser
                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Hendrickson ER,
                                                         standardise OS
                                                                                                                                                                                                                                                                                                        WO200063443-A2.
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Local Sım.
22;
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Matches
                                                                                                          Matches
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                                                                                                                                          요
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                                                                                                                                                                                             spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH28371-AAH28413 represent intergenic spacer target sequences, derived
from Chlamydiaceae. The sequences comprise the intergenic spacer between
the 16S and the 23S rRNA genes, including the far downstream end of the
16S and the far upstream end of the 23S domain I flanking intergenic
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of
                                                                                                                                                                             Intergenic spacer between 16S and 23S rRNA genes of strain FML-16.
                                         ;
0
                         Length 1284;
         Sequence 1284 BP; 392 A; 218 C; 331 G; 343 T; 0 U; 0 Other;
                                         Indels
                                           .
                         DB 4; I
0.00069;
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note= "Domain I of 23S rRNA"
                                          Mismatches
                                                                                                                                                                                                                                                                                                                note= "intergenic spacer"
                         Score 22;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 121-122; 89pp; English.
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                      ACAAGGCCCGAAACGTATTCA 46
                                                          1 ACAAGGCCCGAGAACGTATICA 22
                                                                                                                                                                                                                                                                                                                                                                           959. .1086
/*tag= f
/note= "Region B"
                                                                                                                                                                                                                                                                       |. .221
|*tag= a
|note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                 *tag= e
'note= "23S rRNA"
                                                                                                                                                                                                                                                               "Region A"
                                                                                                                    BP
                                          ö
                                                                                                                    AAH28399 standard; rRNA; 1284
                        100.0%;
illarity 100.0%;
Conservative 0
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/*tag= c
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                                                                                                                                                                                                       infection; ss
                                                                                                                                                                                                                      Chlamydophila pneumoniae
                                                                                                                                                                                                                                                . .537
*tag=
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                                                                                                                                                                                                                                                                 note=
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                     Query Match
Best Local Similarity
Matches 22; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1998;
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                                                                                                                                                   11-SEP-2003
17-SEP-2001
                                                                                                                                                                                              Intergenic
chlamydial
                                                                                                                                                                                                                                       Key
misc_RNA
                                                                                                                                   AAH28399
                                                                                                                                                                                                                                                                                                misc_RNA
                                                                                                                                                                                                                                                                                                                                                                            misc RNA
                                                                                                   RESULT 8
AAH28399/c
                                                                                                                                                                                                                                                                         rRNA
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           and secondarily, a 131 bp region in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 rDNA; dechlorinating activity; chlorinated compound; vinyl chloride; carbontetrachloride; tetrachloroethane; chloroform; dichloromethane; trichloroethane; dichloroethylene; chlorinating bacteria; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etherogenes strain STF, isolated from soil surrounding an industrial site. The 16S rDNA profile is linked to dechlorinating activity.

Bacterial strain comprising the 16S rDNA sequence of the invention are useful for the dechlorination of chlorinated compounds such as carbontetrachloride, tetrachloroethane, chloroform, dichloromethane, tichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics. The 16S rDNA sequence is also useful for identification of new chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence represents the 16S rDNA profile of Dehalococcoides
spacer (referred to as Region.A), and secondarily, a 131 bp region in t 3 end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are useful for identifying and detecting Chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, or to distinguish one strain from another, and for diagnosing chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A 16S rDNA sequence indicative of a chlorinating bacterial strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 1284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1335;
                                                                                                                                                                                                                                                                                                                                    Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1335 BP; 348 A; 288 C; 403 G; 296 T; 0 U; 0 Other;
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100.0%; Pred. No. 0.00069;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 4; I Pred. No. 0.00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 acaaggcccgagaacgrarrca 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240/c
AAC62240 standard; DNA; 1335 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DUPO ) DU PONT DE NEMOURS & CO
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Dehalococcoides ethenogenes.
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Matches
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                                                                                                                                                                                                                                                                                                                                    Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated 16S rDNA sequence indicative of a dechlorinating bacterial organism. The invention is useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in various samples. The method of the invention is useful for identifying a dechlorinating bacterial organism that is a member of a cell population or consortium. The isolated bacterial organism is useful for dechlorinating chlorinated compounds which involves contacting a chlorinated compound with the organism. Oligonucleotide polymer of the invention is useful for separating subfamilies of dechlorinating bacterial organism. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1377 BP; 357 A; 299 C; 415 G; 306 T; 0 U; 0 Other;
                                                                                                                        Dehalococcoides ethenogenes strain DAB 16S rDNA (DHE-DAB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dehalococcoides ethenogenes strain PL 16S rDNA (DHE-PL).
                                                                                                                                            16S rDNA; dechlorinating bacterial organism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16S rDNA; dechlorinating bacterial organism; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
        1322 ACAAGGCCCGAGAACGTATTCA 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dehalococcoides ethenogenes 16S rDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1321 ACAAGGCCCGAGAACGTATTCA 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACAAGGCCCGAGAACGTATTCA 22
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                                                                                                                                                                                                                                                                        8
                                                          AAD57959 standard, DNA, 1377 BP
                                                                                                                                                                                                                                                                                                                                                                             Claim 31; Fig 1; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AADS7957 standard; DNA; 1377 BP
                                                                                                                                                                                                                                                                        (DUPO ) DU PONT DE NEMOURS &
                                                                                                                                                                                                                               30-JAN-2002; 2002WO-US003927
                                                                                                                                                                                                                                                   30-JAN-2002; 2002WO-US003927
                                                                                                                                                                  Dehalococcoides ethenogenes
                                                                                                                                                                                                                                                                                            Ebersole R, Hendrickson E;
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Conservative
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                                                                                                                                                                                                                                                                                                                                                         various samples.
                                                                                                                                                                                      WO2003064695-A1
                                                                                                     20-NOV-2003
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                                                                               AAD57959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                    AAD57959,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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The invention relates to an isolated 16S rDNA sequence indicative of a dechlorinating bacterial organism. The invention is useful for forming probes and primers which are useful for identifying dechlorinating to useful for identifying a dechlorinating bacterial organism that is a member of a cell population or consortium. The isolated bacterial organism that is a involves contacting a chlorinating chlorinated compounds which involves contacting a chlorinated compound with the organism. Oligonucleotide polymer of the invention is useful for separating chlorinating chlorinating chlorinating chlorinating chlorinating subfamilites of dechlorinating bacterial organism. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 22; DB 8; Length 1377; Similarity 100.0%; Pred. No. 0.00069; 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1377 BP; 361 A; 298 C; 412 G; 305 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dehalococcoides ethenogenes strain DLL 16S rDNA (DHE-DLL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16S rDNA; dechlorinating bacterial organism; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                        (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 31; Fig 1; 110pp; English.
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                                                                                                                          30-JAN-2002; 2002WO-US003927.
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AAD57961/c
ID AAD57961 standard, DNA, 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2002; 2002WO-US003927
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                                                                                                                                                                                                                                                                                                                  Hendrickson E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hendrickson E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-636804/60.
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-636804/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 various samples.
WO2003064695-A1
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                                                                                                                                                                                                                                                                                                                     Ebersole R,
                                                             07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD57961;
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Dehalococcoides ethenogenes 16S rDNA
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                                                                                            dechlorinating bacterial organism. The invention is useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in various samples. The method of the invention is useful for identifying a dechlorinating bacterial organism that is member of a cell population or consortium. The isolated bacterial organism is useful for dechlorinating chlorinated compounds which involves contacting a chlorinated compound with the organism.

Oligonucleotide polymer of the invention is useful for separating subfamilies of dechlorinating bacterial organism. The present sequence is behalococcoides ethenogenes 165 rDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in
Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in various samples.
                                                                                      invention relates to an isolated 16S rDNA sequence indicative of a
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                  Length 1377;
                                                                                                                                                                                                                                                         Sequence 1377 BP; 360 A; 300 C; 414 G; 303 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dehalococcoides ethenogenes strain PIN 16S rDNA (DHE-PIN)
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                    Score 22; DB 8; I
Pred. No. 0.00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16S rDNA; dechlorinating bacterial organism; ds.
                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      1321 ACAAGGCCCGAGAACGTATTCA 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                           1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD57960 standard; DNA; 1377 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 31; Fig 1; 110pp; English.
                                                           Claim 31; Fig 1; 110pp; English
                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2002; 2002WO-US003927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dehalococcoides ethenogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hendrickson E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-636804/60.
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003064695-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ebersole R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD57960;
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AAD57960/c
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Involves contacting a chlorinated compound with the organism.

Oligonuclectide polymer of the invention is useful for separating subfamilies of dechlorinating bacterial organism. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                         Gaps
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Pred. No. 0.00069;
Sequence 1377 BP; 357 A; 299 C; 415 G; 306 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1378 BP; 361 A; 300 C; 413 G; 304 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                       Indels
                                             ; Score 22; DB 8; I
; Pred. No. 0.00069;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16S rDNA; dechlorinating bacterial organism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dehalococcoides ethenogenes 168 rDNA
                                                                                                                                                                                                     1321 ACAAGGCCCGAGAACGTATTCA 1300
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                                                                                                                                                             1 ACAAGGCCCGAGAACGTATTCA 22
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                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DUPO ) DU PONT DE NEMOURS & CO
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                                                   100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dehalococcoides ethenogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebersole R, Hendrickson E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2003 (first entry)
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Best Local Similarity 100.
Marches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-636804/60.
                                                Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       various samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003064695-A1
                                                                                                                                                                                                                                                                                                                                                                                                           AAD57958;
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AAC62244/c
ID AAC62
                                                                                                                                                                                                                                                                                                    RESULT 14
AAD57958/c
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us-09-940-860-3.0ligo.rng

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The present sequence represents the 16S rDNA profile of Dehalococcoides ethenogenes strain 195. The 16S rDNA profile is linked to dechlorinating activity. Bacterial strain comprising the 16S rDNA sequence of the invention are useful for the dechlorination of chlorinated compounds such as carbontetrachloride, tetrachloroethane, chloroform, dichloromethane, trichlorocethane, dichlorocethylene, vinyl chloride, and chloroacomatics. The 16S rDNA sequence is also useful for identification of new chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
                                                                                                                     168 rDNA; dechlorinating activity; chlorinated compound; vinyl chloride; carbontetrachloride; tetrachloroethane; chloroform; dichloromethane; trichloroethane; dichloroethylene; chlorinating bacteria; ss.
                                                                                    A 16S rDNA sequence indicative of a chlorinating bacterial strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New 16S rDNA profile derived from Dehalococcoides ethenogenes and indicative of a dechlorinating bacterial strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1443 BP; 379 A; 306 C; 443 G; 314 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 49-50; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                   Ebersole RC;
                                                                                                                                                                                                                                                                                                         13-APR-2000; 2000WO-US009883.
                                                                                                                                                                                                                                                                                                                                            15-APR-1999; 99US-0129511P.
                                                                                                                                                                                                Dehalococcoides ethenogenes
                                                 19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-024581/03.
                                                                                                                                                                                                                                                                                                                                                                                                                   Hendrickson ER,
                                                                                                                                                                                                                                WO200063443-A2
               AAC62244;
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1329 ACAAGGCCCGAGAACGTATTCA 1308

1 ACAAGGCCCGAGAACGTATTCA 22

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Gaps

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Query Match 100.0%; Score 22; DB 4; Length 1443; Best Local Similarity 100.0%; Pred. No. 0.00069; Matches 22; Conservative 0; Mismatches 0; Indels

4, 2004, 06:43:37 Search completed: August Job time : 182.771 secs

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August 4, 2004, 06:43:54; Search time 208.988 Seconds (without alignments) 247.629 Million cell updates/sec
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1: /cgn2 6/ptodata/2/pna/PCT NEW COMB.seq:*
2: /cgn2 6/ptodata/2/pna/USOF NEW COMB.seq:*
3: /cgn2 6/ptodata/2/pna/USO7 NEW COMB.seq:*
5: /cgn2 6/ptodata/2/pna/USO8 NEW COMB.seq:*
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6: /cgn2 6/ptodata/2/pna/USO9 NEW COMB.seq:*
7: /cgn2 6/ptodata/2/pna/USO1 NEW COMB.seq:*
8: /cgn2 6/ptodata/2/pna/USO1 NEW COMB.seq2:*
9: /cgn2 6/ptodata/2/pna/USO1 NEW COMB.seq3:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                     4754066 segs, 1232178907 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                  1 gtgccagcagcagcggtaata 21
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Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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21
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•			SUMMARIES	
Result	بد	Query				
No	Score	Match	Match Length D	DB	OI	Description
υ	1 17	81.0	1542	œ	US-10-864-684-581	Sequence 581, App
υ	2 17	81.0	2838	-	PCT-US03-41761-45189	Sequence 45189, A
υ	3 17	81.0	2838	Н	PCT-US03-41761-45189	Sequence 45189, A
υ	4 17	81.0	2838	Н	PCT-US03-41766A-45189	4518
	5 16	76.2	783	Н	PCT-US03-36229-174	Sequence 174, App
	6 16	76.2	783	Н	PCT-US04-17686-2493	2493
	7 16	76.2	815	9	US-10-425-115-47421	Sequence 47421, A
υ	8 16	76.2	830	9	US-10-425-115-79433	794
	9 16	76.2	1119	9	US-10-669-143-12	12,
_	0 16	76.2	1119	7	US-10-835-208-10	10,
-	1 16	76.2	1647	Н	PCT-US04-05092-48	Sequence 48, Appl
b	2 16	76.2	109725	7	US-10-767-471-10719	
D	.3 15	71.4	201	9	US-10-425-115-139088	
U	.4 15	71.4	213	Н	PCT-US04-12047-347	Seguence 347, App
Ö	.5 15	71.4	260	9	US-10-425-115-49000	49000
υ Π	.6 15	71.4	300	φ	US-10-425-115-44757	Sequence 44757, A
-	.7 15	71.4	526	v	US-10-425-115-139649	
U	.8	71.4	717	ø	US-10-425-115-152690	Seguence 152690,
υ	.9	71.4	748	ø	US-10-425-115-171414	Seguence 171414,
. 1	П	71.4	837	ø	US-10-425-115-146825	Seguence 146825,
	15	71.4	863	ø	US-10-425-115-146920	Sequence 146920,
. 4	г	71.4	923	۲	US-10-767-701-11322	E.
U	3 15	71.4	-	Н	PCT-US04-02974-43	
U	34 15	71.4	1083	7	US-10-770-668-43	Sequence 43, Appl

Sequence 34028, A Sequence 34028, A Sequence 34028, A Sequence 211, App Sequence 179268, Sequence 179268, Sequence 179268, Sequence 29, Appl Sequence 29, Appl Sequence 145, App Sequence 5663, App Sequence 8, Appli			Length 1542; ; Indels 0; Gaps 0;	SYSTEMS FOR INFERRING BOVINE BREED
PCT-US03-41761-34028 PCT-US03-41761-34028 PCT-US03-41766-34028 PCT-US03-41766-34028 PCT-US03-41766-34028 US-10-425-115-109268 US-10-425-115-19268 US-10-425-115-19268 US-10-425-115-19268 US-10-425-115-19268 US-10-425-115-19268 US-10-421-468-79 PCT-US03-117-145 US-10-127-823A-145 US-10-127-823A-145 US-10-127-823A-145 US-10-127-823A-145 US-10-133-117-145 US-10-143-117-145 US-10-183-117-145 US-10-868-184A-5663 US-10-868-184A-5663 PCT-US03-41269-8	ALIGNMENTS	/10864684 zo zia ial Antigens US/10/864,684 06-08 3.1	Score 17; DB 8; ; Pred. No. 9.6; 0; Mismatches 0 19	/TUS0341761 DNS, METHODS, AND CT/US03/41761 60/437,482
71.4 71.4 71.4 71.4 71.4 71.4 71.4 71.4		or control of control	ch 1 Similarity 100.0% 17; Conservative 3 GCCAGCAGCAGGGTAA AB GCCAGCAGCAGGGTAA	45189/c 9, ADPI MI GENOI MI GENOI DENIZE, COSENEE: ROSENEE: HOLM, TI ENTICN: CE: MMI. CC: MMI
. 0 0000 0000 0 0000 0 0 0 0 0 0 0 0 0		RESULT 1 US-10-864-684-581/AP Sequence 581, AP GENERAL INFORMAT APPLICANT: RAF APPLICANT: RAF APPLICANT: RAF APPLICANT: RAF APPLICANT: PIZ APPLICANT: PIZ APPLICANT: PIZ APPLICANT: RAF APPLICANT: PIZ CURRENT FILING APPLICANT: SEQ INWERS OF SEQ INWEST OF SEQ INWERS OF SEQ INWE	Query Match Best Local Si Matches 17; Qy 3 G	SULT 2 Sequen Sequen APPLI APPLI APPLI APPLI APPLI TITLE CURRE CURRE PRIOR NUMBOR

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81.0%; Score 17; DB 1; Length 2838; 100.0%; Pred. No. 9.7; ive 0; Mismatches 0; Indels
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; Sequence 47421, Application US/10425115
; GENERAL INFORMATION:
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                                                                     Local Similarity 100.
18 17; Conservative
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                                    Query Match
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Sequence 45189, Application PC/TUS0341761
Sequence 45189, Application PC/TUS0341761
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APPLICANT: MAI GENOMICS, INC.
APPLICANT: REER, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS, METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100WO
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Pred. No. 9.7;
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Pred. No. 9.7;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US03-41766A-45189/c; Sequence 45189, Application PC/TUS0341766A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEG ID NO 45189
LENGTH: 2838
                                                                                                  TYPE: DNA
CRGANISM: Bovine 19866880933064
PCT-US03-41761-45189
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PCT-US03-41761-45189
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 45189
LENGTH: 2838
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Matches 17; Conservative
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FOLLOWSTING DATE 2493, Application PC/TUS0417686

Sequence 2493, Application PC/TUS0417686

GENERAL INFORMATION:
GENERAL INFORMATION:
THE GOVERNMENT OF HEALTH AND HUMAN SERVICES, CENTERS
APPLICANT: THE SCRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS
APPLICANT: FOR DISEASE CONTROL AND PREVENTION
TITLE OF INVENTION: PUT MICROARRAY AND USES
TITLE OF INVENTION: PUT MICROARRAY AND USES
CURRENT APPLICATION NUMBER: PCT/US04/17686
CURRENT FILING DATE: 2003-06-04
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 3085
SEGFWARE PAECHIN VERSION 3.2
SEQ ID NO 2493
LENGTH: 783
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                                                                                                                                                                                                                                                                                                          APPLICANT: NUCLEAR INC.
TITLE OF INVENTION: Therapeutic and Screening Methods
FILE REFERENCE: 50001/014W02
CURRENT RPILICATION NUMBER: PCT/US03/36229
CURRENT RILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/426,305
PRIOR APPLICATION NUMBER: 60/426,305
PRIOR PLING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 198
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 174
LENGTH: 783
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Sequence 10, Application US/10835208
GENERAL INFORMATION:
APPLICANT: Rosanne M. Crooke
APPLICANT: Rosanne M. Crooke
TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
CURRENT APPLICATION NUMBER: US/10/835,208
CURRENT PILING DATE: 2004-04-29
PRIOR PILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 1119
                                                                                               APPLICANT: Christopher J. Kirk
APPLICANT: Simon X. Xie
APPLICANT: Simon X. Xie
APPLICANT: Simon X. Xie
APPLICANT: Simon X. Xie
APPLICANT: Agnes Choppin
TITLE OF INVENTION: Targeted Gene Disruptions, Compositions
TITLE OF INVENTION: Targeted Gene Disruptions, Compositions
TITLE OF INVENTION: Targeted Gene Disruptions, CURRENT OF INVENTION: And Methods Related Thereto
FILE REFERENCE: R-De1.3
CURRENT FILING DATE: 2003-09-23
CURRENT FILING DATE: 2002-09-24
PRIOR FILING DATE: 2002-09-24
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Pred. No. 31;
0; Mismatches (
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12
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76.2%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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                                         Thomas J. Brennan
Catherine Guenther
Robert Klein
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Best Local Similarity 100.0
Matches 16; Conservative
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CRGANISM: Mus musculus
US-10-669-143-12
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; LOCATION: (33)...(815)
US-10-835-208-10
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US-10-835-208-10
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-4-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 47421
LENGTH: 815
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US-10-425-115-79433, Application US/10425115

Sequence 79433, Application US/10425115

Sequence 79433, Application US/10425115

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: 2003-04-28

NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_143255C.1
US-10-425-115-47421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Clone ID: MRT4577_172470C.1 US-10-425-115-79433
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (1)..(815)
OTHER INFORMATION: unsure at all n locations
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(WS-10-669-143-12)
(Sequence 12, Application US/10669143)
(GENERAL INFORMATION:
APPLICANT: William Matthews
APPLICANT: Rassell Phillips
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Russell Phillips
Michael V. Wiles
Thadd C. Reeder
Robert G. Wisotzkey
Keith D. Allen
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APPLICANT:
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APPLICANT:
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71.4%; Score 15; DB 6;
100.0%; Pred. No. 97;
tive 0; Mismatches
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US-10-425-115-139088
Sequence 139088, Application US/10425115 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 347, Application PC/TUS0412047 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
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Sequence 10719, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01505
FURRENT APPLICATION NUMBER: US/10/767,471
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FASELSEQ for Windows Version 4.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: INCTIC CORPORATION; RAMKUMAR, Jayalaxmi;
APPLICANT: INCTIC CORPORATION; RAMKUMAR, Jayalaxmi;
APPLICANT: CHAMLA, Narinder K.; TRAN, Uyen K.;
APPLICANT: GENERAL, Shanya; LEE, Soo Yeun;
APPLICANT: HEGHA, Shanya; LEE, Soo Yeun;
APPLICANT: KHARE, Reena; JIANG, Xin;
APPLICANT: GRANB, April J.A.; RICHREDSON, Thomas;
APPLICANT: GRANB, April J.A.; RICHREDSON, Thomas;
APPLICANT: GRANB, Ann
ITLE OF INVENTION: KINASES AND PHOSPHATASES
FILE REPERENCE: PP-1643 PCT
CURRENT APPLICATION NUMBER: DCT/USO4/05092
CURRENT PILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US 60/449,059
PRIOR FILING DATE: 2003-02-20
PRIOR PLING DATE: 2003-03-19
PRIOR PLING DATE: 2003-03-19
PRIOR FILING DATE: 2003-04-09
PRIOR FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PERE PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7523794CB1
PCT-USO4-05092-48
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Best Local Similarity 100.
Matches 16; Conservative
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ORGANISM: Homo sapiens
US-10-767-471-10719
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ORGANISM: Homo sapiens
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US-10-767-471-10719/c
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LENGTH: 109725
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SEGUENCE 34, APPLICATION FRIENDEMENTICS, INC.

TITLE OF INVENTION: HUMAN POLYMEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HUMAN POLYBER OF SEC IN ORIGINAL PRINCE OF SEC IN OR SEC IN ORIGINAL
APPLICANT: La Rosa, Thomas J.
APPLICANT: As Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: 18-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NO 139088
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CORGANISM: Homo sapiens
PCT-US04-12047-347
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Best Local Similarity
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VS-10-45-115-49000/c

VS-10-45-115-49000/c

Sequence 49000, Application US/10425115

Sequence 49000, Application US/10425115

Sequence 49000, Application US/10425115

Sequence 49000, Application US/10425115

APPLICANT: Every Thomas J.

APPLICANT: Applicant Solution States

TITLE OF INVENITON: Plants

TITLE OF INVENITON: Plants

TITLE OF INVENITON: Plants

TITLE OF INVENITON: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 49000

LENGTH: 260
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0; Indels
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CRCANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_144694C.1

US-10-425-115-49000
0; Mismatches
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15; Conservative
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August 4, 2004, 06:32:11; Search time 1917.07 Seconds (without alignments) 385.436 Million cell updates/sec
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/cgn2_6/ptodata/2/pna/US100A_COMB.seq:
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Gaps

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Length 21; Indels

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Query Match
100.0%; Score 21; DB 39;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 21; Conservative 0; Mismatches 0;
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-4
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US-60-128-439-5333

US-60-128-439-2909

US-60-128-439-2001

US-60-128-439-3001

US-60-128-439-3001

US-60-128-439-3001

US-60-128-439-3001

US-60-128-439-3001

US-60-128-439-3001

US-60-128-439-3001

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US-60-128-439-3001
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S-60-128-439-4162
S-09-540-235-453
S-60-128-439-679
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US-09-540-235-4801
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US-60-128-439-3924
US-09-540-235-3911
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-60-128-439-1726
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-60-128-439-4897
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                                          Query
Match Length
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ALIGNMENTS

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Sequence 4, Application US/09940860
GENERAL INFORMATION:
APPLICANT: Rothman. Richard;
APPLICANT: Madimidar, Maulik
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FILE REFERENCE: 01107.0018 S
CURRENT FILING DATE: 2001-08-29
FILE REPLICATION NUMBER: 06/229,376
FRIOR APPLICATION NUMBER: 60/229,376
FRIOR APPLICATION NUMBER: 60/229,376
FRIOR APPLICATION NUMBER: 60/229,376
FRIOR PILING DATE: 2000-08-31
SEQ ID NO 4
SEQ ID NO 4
ENGREE FASTSEQ FOR WINGOWS VERSION 4.0
RESULT 1
US-09-940-860-4
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TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

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RESULT 2
US-09-369-922-1
; Sequence I. Application US/09369922
; GENERAL INFORMATION:
APPLICANT: Ting Robert C.
APPLICANT: Ting Robert C.
APPLICANT: Tham, Jill M.
APPLICANT: Tham, Jill M.
APPLICANT: Theresa M.
TITLE OF INVENTION: Extrachromosomal Genetic Material
TITLE OF INVENTION: Extrachromosomal Genetic Material
TITLE OF INVENTION: Diagnosis of Plasmodium Infection by Analysis of
TITLE OF INVENTION: Diagnosis of Plasmodium Infection by CURRENT TILL MEDICATION NUMBER: US/09/369,922
CURRENT APPLICATION NUMBER: PCT/IB98/00212
FRIOR APPLICATION NUMBER: AU P09481/97
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-04-21
FRIOR PLING DATE: 1997-04-21
FRIOR FILING DATE: 1997-04-21
FRIOR FILING DATE: 1997-04-21
FRIOR FILING DATE: 1997-04-21
FRIOR SEQIE DATE: 1997-04-21
FRIOR FILING DATE: 1997-04-21
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GENERAL INFORMATION:

APPLICANT: ATA, Anna K.

APPLICANT: Ting, Robert C.

APPLICANT: Ting, Robert C.

APPLICANT: Tham, Jill M.

APPLICANT: Tham, Jill M.

APPLICANT: Tham, Jill M.

APPLICANT: Tham, Jill M.

TITLE OF INVENTION: Diagnosis of Parasites
FILE REPERENCE: 64-99

CURRENT APPLICATION NUMBER: US/09/369,992C

CURRENT PILLING DATE: 1999-00-06

PRIOR PILLING DATE: 1998-02-05

PRIOR PILLING DATE: 1997-09-26

PRIOR PILLING DATE: 1997-04-21

PRIOR PILLING DATE: 1997-04-21

PRIOR PELICATION NUMBER: AU PO9481/97

PRIOR PELICATION NUMBER: AU PO94329/97

PRIOR PELING DATE: 1997-04-21

PRIOR PELING DATE: 1997-04-21

PRIOR PELING DATE: 1997-04-21

PRIOR PELING DATE: 1997-04-21

PRIOR PELING DATE: 1997-02-06
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CRGANISM: Plasmodium berghei
US-09-369-922-1
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US-09-369-992C-1
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Pricher, Dane K.

APPLICANT: Lalgudi, Raghuath V.
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses:
TITLE OF INVENTION: thereof
TITLE OF INVENTION: 18-22(15749)B
CURRENT APPLICATION NUMBER: US/09/540,235
CURRENT PILING DATE: 2000-04-03
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5333
LENGTH: 239
TYPE: Name
                                                             Sequence 4848, Application US/60128439
GENERAL INFORMATION:
APPLICANT: Fisher, Dane K.
APPLICANT: Flagudi, Raghunath V.
TITLE OF INVENTION: Uncleic Acid Sequences from Cyanidium caldarium and Uses TITLE OF INVENTION: thereof FILE REPRENEUS: 30-21(15749) A CURRENT APPLICATION UNMER: US/60/128,439
CURRENT FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5661
EENGTH: 195
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Sequence 3158, Application US/60128439
Sequence 3158, Application US/60128439
GENERAL INFORMATION:
APPLICANT: Fisher, Dane K.
APPLICANT: Lalgudi, Radhunath V.
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: thereof
FILE REFERENCE: 38-21(15749)A
FILE REFERENCE: 38-21(15749)A
CURRENT APPLICATION UNMBER: US/60/128,439
CURRENT FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5661
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CRGANISM: Cyanidium caldarium
CTHER INFORMATION: Clone ID: LIB190-062-Q1-E1-E12
US-09-540-235-5333
                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION; Clone ID: LIB190-062-Q1-E1-E12
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100.0%; Pred. No. 62;
iive 0; Mismatches 0
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: thereof
FILE REPERENCE: 38-21(15749)B
CURRENT APPLICATION NUMBER: US/09/540,235
CURRENT FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
SEQ ID NOS: 5674

LENGTH: 116
TYPE: ...
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Sequence 3619, Application US/60128439

Sequence 3619, Application US/60128439

SENERAL INFORMATION:
APPLICANT: Ladyadi, Raghunath V.
TITLE OF INVENTION: Naclaic Acid Sequences from Cyanidium caldarium and Uses;
TITLE OF INVENTION: thereof
TITLE OF INVENTION: thereof
TITLE OF INVENTION: US/60/128,439

CURRENT APPLICATION NUMBER: US/60/128,439

CURRENT PILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 5661

LENGTH: 108
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68;
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) OTHER INFORMATION: Clone ID: LIB190-049-Q1-E1-B2
US-09-540-235-4801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Clone ID: LIB190-049-Q1-E1-B2 US-60-128-439-3619
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                                                             TYPE: DNA
; ORGANISM: Plasmodium berghei
US-09-369-992C-1
SOFTWARE: Patentin Ver. 2.0
           SEQ ID NO 1
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Matches
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137 GTGCCAGCAGCAGCGGTAA 155
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APPLICANT: Lalgudi, Raghunath V.

TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses TITLE OF INVENTION: thereof Sequences from Cyanidium caldarium and Uses FILE REFERENCE: 38-21(15749)B

CURRENT APPLICATION NUMBER: US/09/540,235

CURRENT FILING DATE: 2000-04-03

PRIOR FILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO : 1015
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fisher.
APPLICANT: Lalgudi, Raghunath V.
TITLE OF INVENTION: Nacleic Acid Sequences from Cyanidium caldarium and Uses:
TITLE OF INVENTION: thereof
TITLE OF INVENTION: thereof
FILE REFERENCE: 38-21 (15749) NS (60/128,439
CURRENT APPLICATION NUMBER: US/60/128,439
NUMBER OF SEQ ID NOS: 5661
SEQ ID NO 2009
LENGTH: 287
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61;
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Pred. No. 61;
                                                                                                                                                                                                  0; Indels
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                                                                                              ; OTHER INFORMATION: Clone ID: LIB190-043-Q1-E1-C12
US-60-128-439-3158
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) OTHER INFORMATION: Clone ID: LIB190.040-Q1-E1-B11

VGS-60-128-439-2909
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100.0%; Pred. No. 61;
iive 0; Mismatches 0
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OCGANISM: Cyanidium caldarium
COTHER INFORMATION: Clone ID: LIB190-019-Q1-E1-H1
US-09-540-235-1015
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100.0%; Pred. No. c...
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Best Local Similarity 100.0%; P.
Matches 19; Conservative 0;
                                      TYPE: DNA ORGANISM: Cyanidium caldarium
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ORGANISM: Cyanidium caldarium
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Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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US-09-540-235-1015
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SEQ ID NO 3158
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Sequence 4226, Application US/09540235
GENERAL INFORMATION:
APPLICANT: Fisher, Dane K.
APPLICANT: Lalgudi, Raghunath V.
TITLE OF INVENTION:
TITLE OF INVENTION: thereof 3.21(15749)B
TITLE OF INVENTION: UNMERR: US/09/540,235
CURRENT APPLICATION NUMBER: US/09/540,235
CURRENT FILING DATE: 2000-04-03
PRIOR PELING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4526
LENGTH: 300
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APPLICANT: Lalgudi, Raghunath V.
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: thereof
FILE REFERENCE: 38-21(15749)B
                                                  APPLICANT: Fisher, Dane K.
APPLICANT: Fisher, Dane K.
APPLICANT: Lalgudi, Raghumath V.
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: thereof
FILE REPERENCE: 38-21(15749)A
CURRENT APPLICATION NUMBER: US/60/128,439
CURRENT FILING DATE: 1999-04-06
SEQ ID NOS: 5661
LENGTH: 295
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90.5%; Score 19; DB 68; Length 295;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels
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Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA

CRGANISM: Cyanidium caldarium

CTHER INFORMATION: Clone ID: LIB190-040-Q1-E1-B11

US-09-540-235-4526
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB190-019-Q1-E1-H1
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CURRENT APPLICATION NUMBER: US/09/540,235
Sequence 1486, Application US/60128439 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GTGCCAGCAGCAGCGGTAA 19
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Best Local Similarity 100.0%; Pi
Matches 19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Cyanidium caldarium
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US-09-540-215-4659

US-09-540-215-4659

Sequence 4659, Application US/09540235

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION:
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US-60-128-439-5580
US-60-128-439-5580

Sequence 5580, Application US/60128439

GENERAL INFORMATION:
APPLICANT: Fisher, Dane K.
APPLICANT: Fisher, Dane K.
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: thereof
TITLE OF INVENTION: thereof
TITLE OF INVENTION UNDER: US/60/128,439
CURRENT APPLICATION NUMBER: US/60/128,439
CURRENT FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5661
LENGTH: 301
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90.5%; Score 19; DB 23; Length 302;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

90.5%; Score 19; DB 23; Length 301;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels
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CGANIGM: Cyanidium caldarium

COTHER INFORMATION: Clone ID: LIB190-043-Q1-E1-C12

US-09-540-235-4659
                                                                                                                                                                                                                                              TYPE: DNA

OGGANISM: Cyanidium caldarium

OTHER INFORMATION: Clone ID: LIB190-071-Q1-E1-G6

US-09-540-235-3580
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US-60-128-439-5580
                                            60/128,439
                                                             . 1999-04-06
5674
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        2000-04-03
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ORGANISM: Cyanidium caldarium
FEATURE:
CURRENT FILING DATE: 2000-
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 3580
LENGTH: 301
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TYPE: DNA
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Sequence 2320, Ap
Sequence 7428, Ap
Sequence 7487, Ap
Sequence 11, Appl
Sequence 11, Appl
Sequence 9158, Ap
Sequence 958, App
Sequence 1269, Ap
Sequence 1269, Ap
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1, Appli
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3, Appli
4926, Ap
                                                              August 4, 2004, 06:01:54; Search time 37.9518 Seconds (without alignments) 307.073 Million cell updates/sec
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Sequence 2,
Sequence 1,
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Sequence
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/pcTus_comp.*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-7428
US-09-252-991A-74209
US-09-807-784B-11
US-09-807-784B-11
US-09-621-976-1953
US-09-621-976-9153
US-09-621-976-9153
US-09-621-976-9153
US-09-80-039A-4976
US-09-252-991A-1129
US-09-861-038A-1
US-09-147-915-1
US-09-147-915-1
US-09-147-915-1
US-09-184-001-3
US-09-184-001-3
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US-08-554-612C-35
US-08-721-458B-67
US-08-721-458B-68
US-08-554-612C-37
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US-09-596-002-41
US-09-103-840A-2
US-09-103-840A-1
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                                                                                                                                                                                      682709 segs, 277475446 residues
                                          OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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seq length: 200000000
                                                                                                           US-09-940-860-4
21
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Match Length
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Perfect score:
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No.
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RESULT 2
US-08-328-352-2320
Sequence 2320, Application US/09328352
Patent No. £552958
GENERAL INFORMATION:
Patent No. £562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BUMMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OP SEQ ID NOS: 8252
SEQ ID NO 2320
LENGTH: 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pacquence 7151, Application US/09252991A

Pacquence 7151, Application US/09252991A

Pacquence 7151, Application US/09252991A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (256)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7151
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                       Sequence 538, App
Sequence 181, App
Sequence 181, App
Sequence 3580, Ap
Sequence 9188, Ap
Sequence 9188, Ap
Sequence 9188, Ap
Sequence 1668, Ap
Sequence 1668, Ap
Sequence 1661, Ap
                                                                                                                                                                                                                                                                                                   269, App
1151, Ap
15, Appl
15946, A
156, A
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     Sequence Sequence Sequence
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US-08-554-612C-48
US-09-621-976-538
US-09-621-976-538
US-09-107-532A-181
US-09-621-976-3580
US-09-252-991A-066
US-09-252-991A-0488
US-09-252-991A-0688
US-09-252-991A-0688
US-09-252-991A-10611
US-09-621-976-3656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
LOCATION: (256)
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76.2%; Scc.
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Best Local Similarity 100.0
Matches 16; Conservative
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GENERAL INFORMATION:
APPLICANT: Tanuma, Sei-ichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                             Conservative
                                  Local Similarity
hes 16; Conserv
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NAME/KEY: unsure
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US-09-807-784B-11/c
                 Query Match
Best Local S:
Matches 16
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Sequence 7209, Application US/09252991A

Sequence 7209, Application US/09252991A

Sequence 7209, Application US/09252991A

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR PLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7209

LENGTH: 2541
                                                                                                                                                                                                                                                                                                                US-09-252-991A-7428/c

Sequence 7428 Application US/09252991A

Sequence 7428 Application US/09252991A

Sequence 7428 Application US/09252991A

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVERTION:

TITLE OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVERTION: ABERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1998-02-18

FRICR APPLICATION NUMBER: US 60/074,788

PRICR APPLICATION NUMBER: US 60/094,190

PRICR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7428
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LOCATION: (2058)

CHER INDEMATION: Identity of nucleotide at the above locations are unknown.

478-09-252-991A-7209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . LOCATION: (422)
, OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7428
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                                                                                   Score 16; DB 4; Length 684;
Pred. No. 10;
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                                                                                     Query Match 76.2%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 10; Matches 16; Conservative 0; Mismatches
                   , ORGANISM: Acinetobacter baumannii
US-09-328-352-2320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                               170 CAGCAGCAGCGGTAAT 185
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Best Local Similarity
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NAME/KEY: unsure
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US-09-252-991A-7487/C
US-09-252-991A-7487/C
US-09-252-991A-7487/C
US-09-252-991A-71LE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/22, 991A

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7487

LENGTH: 3099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shiokawa, Daisuke
TITLE OF INVENTION: No. 6653118el Deoxyribonuclease, Gene Encoding Thereof and Use Th
FILE REFERENCE: 210792
CURRENT PELLOTATION NUMBER: US/09/807, 784B
CURRENT PILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: JP 11-230870
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 15
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1117)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Score 16; DB 4; Length 2541;
Pred. No. 10;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.2%; Score 16; DB (100.0%; Pred. No. 10; iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                             1848 Greechechechece 1863
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GENERAL INFORMATION:
APPLICANT: NO. C.J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1269
LENGTH: 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4976, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMOVOLAR FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMOVOLAR FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342

LENGTH: 628
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                                                                                                                                                                                        Length 558;
                                                                                                                                                                                        Query Match 71.4%; Score 15; DB 4; Best Local Similarity 100.0%; Pred. No. 32; Matches 15; Conservative 0; Mismatches (
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; Sequence 1269, Application US/09252991A
; Patent No. 6551795
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US-09-252-991A-1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae US-09-489-039A-4976
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 958
LENGTH: 558
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                                                                                                                                                                                                                                                                                                                                   231 AGCAGCAGCGGTAAT 217
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                           ; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-958
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US-09-489-039A-4976
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                                                                                      1S-09-540-236-1498/c
Sequence 1498, Application US/09540236
Sequence 1408, Application US/09540236
Sequence 1408, Application US/09540236
GENERAL INFORMATION:
GENERAL INFORMATION:
CHAPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND THERAPBUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
FILE REPRESENTE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NOS: 3840
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Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 2709, 2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
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32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9153, Application US/09621976
Patent No. 6639063
GRUERAL INPORMATION:
APPLICANT: Unmas Milhe Edwards, J.B.
APPLICANT: Glocker, S.
APPLICANT: Glocker, S.
TITLE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9153
LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.4%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 32; Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 15; DB 100.0%; Pred. No. 32; cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 320
OTHER INFORMATION: n=a, g, c or t
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  32 TGCCAGCAGCAGCGG 18
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
Catarrhalis
US-09-540-236-1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-09-621-976-9153/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-540-236-958/c
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                                                             71.4%; Score 15; DB 3; Length 1575; 100.0%; Pred. No. 32; 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,034B
FILING DATE: 18 -MAY-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: JOHNSTON NUMBER: 35,910
REGISTRATION NUMBER: 35,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%; Scorc
100.0%; Pred. No. 52,
... 0; Mismatches
                                                                                                                                                                                                                               RESULT 14
US-09-861-034B-1/C
Sequence 1, Application US/09861034B
Patent No. 6569429
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
Baron, Will F.
TITLE OF INVENTION: Human DNase II
NUMBER OF SEQUENCES: 10
CORRESPONDENCE DDRESS: 1
STREET: 1 DNA WAY
STREET: 1 DNA WAY
COUNTRY: COULT SOUTH SAN Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P1024D1
TELECOMMUNICATION INFORMATION:
TELEPRAN: 650/225-3862
TELEPRAX: 650/952-9881
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-861-034B-1
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APPLICANT: Eastman, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1575 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                             106 receaseascases 92
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                                                               Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 15; Conservative
               ; MOLECULE TYPE: DNA
US-08-639-294-1
 Linear
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US-09-147-915-1/c
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPEKATING SISTEM: E-LOGYES-LOG
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,294
FILING DATE: 25-Apr-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JOHNSTON, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: 91024
TELECHOME: 415/225-3562
TELECHAN: 415/922-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Barcon, Will F.
IITLE OF INVENTION: Human DNase II
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-639-294-1/c; Sequence 1, Application US/08639294; Patent No. 6265195
                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                   818 CCAGCAGCAGCGGTA 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       868 CCAGCAGCAGCGGTA 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CCAGCAGCAGCGGTA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 15; Conservative
LENGTH: 1575 base | TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                     임
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### APPLICANT: Krieser, Ronald
### TITLE OF INVENTION: Decoxyribonuclease II Proteins and cDNAs
### FILE REFERENCE: DC-008
### CURRENT PILICATION NUMBER: US/09/147,915A
### CURRENT FILING DATE: 1999-03-23
### EARLIER PILING DATE: 1999-10-15
### EARLIER PILING DATE: 1997-10-09
### EARLIER PILING DATE: 1996-10-15
### FARLIER PILING DATE: 1996-10-15
### CONTANTE: PatentIN Ver. 2.0
### SEQ ID NO 1
### SEQ ID NO 1
### SEQ ID NO 1
### CONTANTE: DATE: DATE: 1995-10-15
### CONTANTE: DATE: DA
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Database

Searched:

Scoring table:

Perfect score:

Title:

Sequence:

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BIG97005 [KS2210.7]
BIG97004 [KS2210.7]
BIG97004 [KS2210.7]
BIG97004 [KS2210.7]
BIG97004 [KS2210.7]
BIG97004 [KS2210.7]
BIG9733 [K71806.7]
BIG9733 [K71806.7]
BIG9733 [K71806.7]
BIG973 [K9201.X]
BIG9704 [K9201.X]
BIG9707 [K9200.X]
BIG9707 [K9200.X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALGESTAL SEPERGILLUS DE MENA linear EST 19-OCT-195 X2gO2ai.f1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone X2gO2ai 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Farrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Burotiales; Trichocomaceae; Emericella.

1 (bases 1 to 213)

1 (Xupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R. and Roe, B.

A Aspergillus nidulans EST Database
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emericella nidulans (anamorph: Aspergillus nidulans)
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                                                                                                                                                  BM156391
B1533213
BM162093
B1866999
B1708149
B1866073
BM102773
A1087773
AN281772
B187773
AW281793
B1708185
B170
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CB6678345
BZ067895
BZ067045
CD857812
CD857812
CD85743
CD857443
CD857443
CD8576671
CD856671
CD856673
CD856773
CD
                                               BI897005
BI897004
AA784579
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BF064383 SWOVAFCAP
AIS85049 fb69g07.x
AI211182 00c05a1.f
                                                                                                                                                                                 4, 2004, 05:41:25; Search time 1532.58 Seconds (without alignments) 428.668 Million cell updates/sec
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Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                         GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                 OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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EST 19-0CT-1998

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Score

Result No.

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Danio rerio
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                                                                                                                                                                                                          셤
                                                                                                                                                                                                      /tissue type="vegetative mycelia, asexual structures" /clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda and library" /note="Vector: pBlueScript SK-; Site_l: EcoRi; Site_2: XhoI; 5, end of cDNA cloned into EcoRI site of pBluescript 3, end of cDNA cloned into XhoI site of pBluescript"
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CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onchocerca volvulus
Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF064383
SWOVAFCAP48BIISK Onchocerca volvulus adult female cDNA
(SAM98MIW-OVAF) Onchocerca volvulus cDNA clone SWOVAFCAP48BII 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outracts steer A. Williams

Contacts steer A. Williams

Molecular Parasitology
Smith College Department of Biological Sciences

Smoth College Department of Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA

Tel: 4135853786

Fax: 4135853786

Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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1 (bases 1 to 258)
Lizotte-Wanliewski,M. and Williams,S.A.

Genes expressed in adult female stage of Onchocerca volvulus Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev stage="adult"
/lab_host="XL1-Blue MRF'"
/clone lib="Onchocerca volvulus adult female cDNA
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                                                                                                                                                                                                                                                                                                                                                                                         72.7%; Score 16; DB 9; Length 213; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                               /organism="Emericella nidulans"
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/db_xref="taxon:6282"
/clone="SWOVAFCAP48B11"
/sex="female"
                                                                                                                                                                  /db_xref="taxon:162425"
/clone="x2g02a1"
Seq primer: M13-20
High quality sequence stop: 88.
Location/Qualifiers
                                                                                                                    /mol_type="mRNA"
/strain="FGSC A26"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
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Danio Terio
Danio Terio
Danio Terio
Danio Terio
Danio Terio
Danio Netazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Actinopterygi; Neopterygi; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (Dases 1 to 262)
Eddy, S., Hiller,L., Kucaba,T., Martin,J., Beck,C., Walie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Raterston,R. and Wilson,R.
Upublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Fax: 314 286 1800
Fax: 314
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Eb69g07.xl Zebrafish WashU MPING EST Danio rerio cDNA clone
MAMCE:3717180 3', mRNA sequence.
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zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'tissue_type="26 somite embryos, adult livers, shield
from Dr.Steven A. Williams, email: genome@smith.edu."
                                                                                                                                                                                      Gaps
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0
                                                                                                    Length 258;
                                                                                                                                                                                  0; Indels
                                                                                                            10;
                                                                                                        ore 16; DB |
Pred. No. 32;
Mismatches
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/lab_host="XL1-blue MRF"
                                                                                                            Score 16;
Pred. No.
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/db_xref="taxon:7955"
/clone="IMAGE:3717180"
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                      102 CCCGAGAACGTATTCA 87
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                                                                                                            72.78;
                                                                                                            Query Match
Best Local Similarity 100.
Matches 16; Conservative
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Danio rerio (zebrafish)
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Onchocerca volvulus
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Best Local Similarity 100.
Matches 16; Conservative
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/mol type="mRNA"
/mol type="mRNA"
/dolarielecani62425"
/done="00005a1"
/clone="00005a1"
/clone lib="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/note="vecror: pBlueScript SK-; Site 1: EORI; Site_2:
/note="vecror: pBlueScript SK-; Site 1: EORI; Site_2:
/note cDNA cloned into XhoI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"
analysis were selected following oligonuclectide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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205 bp mRNA linear EST 19-OCT-199
000581-11 Aspergillus nidhlans 24hr asexual developmental and
vegetative CDNA lambda zap library Emericella nidhlans CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: M13-20
High quality sequence stop: 219.
Location/Qualifiers
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Unpublished (1998)
Other ESTS: 00c05al.rl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
Prade,R. and Roe,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emericella nidulans (anamorph: Aspergillus nidulans)
Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trithocomaceae; Emericella.
1 (bases 1 to 285)
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0
                                                                                                                                                                                                                                                          Ouery Match 72.7%; Score 16; DB 9; Length 262; Best Local Similarity 100.0%; Pred. No. 33; Matches 16; Conservative 0; Mismatches 0; Indels
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AI211182.1 GI:3773124
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Conservative 0
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Best Local Similarity
Matches 16; Conserv
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AI211182/c
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AUTHORS
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JOURNAL
COMMENT
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DETRING (SWOAPCRP200015K Onchocerca volvalus achil female cDMA (SANDSMINA-OAR) CONChocerca (SANDSMINA-OAR) (SANDSMINA-OAR) CONCHOCERCA (SANDSMINA-OAR) (SANDSMINA
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Washington University School of Medicine
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BI897004
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Best Local Similarity
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BI897004/c
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JOURNAL
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled 26-somite embryos"
/lab host="Mixed"
/lab host="XL1-blue MRF"
/clon=lib="Ebrafish ICRFzfls"
/clon=strand cloud was primed with a Not I - oligo(dT)15 primer
[5.pdACTAGTTCARGATGGGAGGCCCTTTTTTTTTTTTTTTT], on
mRNA from pooled 26 somite zebrafish embryos;
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloud into the Not I and Sal I
sites of the pSPOTT vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max
Planck Institut fuer Molekulare Genetik, Berlin) and was
not biochemically normalised. 70,000 cloues from this
library were arrayed on high density filters and
subsequently screened by oligomucleotide hybridization
fingerprinting to identify unique or minimally redundant
clones for more intensive analysis."
          Clark, M., Lehrach, H., Appel, B., Eisen, J., Johnson, S., Marra, M., Edark, M., Lehrach, H., Allen, M., Bowles, L., Johnson, S., Marra, M., Joydos, S., Kucaba, T., Lacy, M., Le, M., Lennon, G., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Washu Zebrafish EST Project
Unpublished (1997)
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fk52e10.yl Zebrafish 15-19hr embryonic CDNA Danio rerio CDNA 5',
                                                                                                                                                                                                                                                                             Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wastl.edu

Steve Johnson lab internal ID - P1 89 NOTE - For this library, the CLONE id field represents a position identifier on the original CDNA library preparation. Matthew CLARX: CDNA Library preparation. Matthew CLARX: CDNA Library Arrayed by: Matthew Clarx: CDNA Library Arrayed by: Mashington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare Seq primer: -40ml3 ET from Amersham

High quality sequence stop: 315.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
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                                                                                                                                                                                                              Contact: Steve Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="3D9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AAGGCCCGAGAACGTA 18
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Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptee, M., Theising, B., Allen, N., Bowers, Y., Person, B., Swaller T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Watter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watterston, R. and Wilson, R. Wackerston, R. and Wilson, R. Unpublished (1998)

U published (1998)

U published (1998)

Contact: Stephen L. Johnson Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Fax: 314, 286, 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
rerio cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bmail: zbrafish@watson.wustl.edu
Library constructed by: Bernhard Korn DNA Sequencing by: Washington
University Genome Sequencing Center Clone distribution:
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E.Coli (DHIOB/XL2blue)"
/clone lib="Zebrafish 15-19hr embryonic cDNA"
/note="Vector: pSPORT1; Site_1: Not1; Site_2: SalI; This Zebrafish library was constructed by Dr. Bernhard Korn (email: b.korn@dkfz-heidelberg.de). RZPD library number: 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinicaes: Cyprinidae; Danio.

1 (bases 1 to 371)
1 (bases 1 to 371)
1 Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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/lab_host="E.Coli (DH10B/XL2bl)
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/organism="Danio rerio"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: T3 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="unspecified"
/db_xref="taxon:7955"
/sex="mixed"
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Contact: Stephen L. Johnson
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Fri Aug

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tissue
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Best Local Similarity
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AUTHORS
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KEYWORDS
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                                                                                                                        ORIGIN
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                                                     Email: zbrafish@watson.wustl.edu
Library constructed by: Bernhard Korn DNA Sequencing by: Washington
University Genome Sequencing Center Clone distribution:
RessourcenZentrumprimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                 zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
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/db xref="transpronsings"
/dev stage="15-19 hour embryo"
/dev stage="15-19 hour embryo"
/lab host="E.Coli (DH10B/XL2blue)"
/clone lib="Zebrafish 15-19hr embryonic cDNA"
/note="Vector: pSPORT1; Site_1: Not1; Site_2: SalI; This Zebrafish library was constructed by Dr. Bernhard Korn (email: b.korn@dkfz-heidelberg.de). RZPD library number: 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1377 bp mRNA linear EST 29-JUL-1994 fib09al.fl Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone fib109al 3', mRNA sequence.
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Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

1 (bases 1 to 377)

Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry.
Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA
Fat: 405 325 4912
Fax: 405 325 7762
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prade, R. and Roe, B.
An Aspergillus nidulans EST Database
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: broe@ou.edu
We anticiphate the future release of
Genetics Stock Center
Seq primer: M13-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.7%; Score 16; DB 100.0%; Pred. No. 34; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="flh09a1"
                                                                                                                                                                                                                                                                                         /organism="Danio rerio"
/mol_type="mRNA"
/strain="unspecified"
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Location/Qualifiers
                                                                                                                                                                                                                             Seq primer: T7 from Gibco.
Location/Qualifiers
1. .371
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AA784579.1 GI:2844747
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                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                             rerio cDNA
                                                                                                                                               www.rzpd
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AA784579/c
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Danjo rerio

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

(Ypriniformes; Cyprinidae; Danio.

(Selection, R., Steptoe, M., Tehrach, H., Lee, R., Li, F., Marra, M.,

(Inderwood, K., Steptoe, M., Tehraising, B., Allen, M., Bowers, Y.,

(Inderwood, K., Steptoe, M., Tehising, B., Allen, M., Bowers, Y.,

(Inderwood, K., Steptoe, M., Tehising, B., Allen, M., Bowers, Y.,

(Inderwood, K., Shaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

(Interest), Rahin, T., Jackson, Y., Cardenas, M., McCann, R.,

(Interpretation, R., Pape, D., Harvey, N., Schurk, R.,

(Intermit Estra: fc43d0.yl

(Contact: Stephen L. Johnson

(Nashington University School of Medicine

(A444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810

Fax: 314 286 1810

Fax
/tissue_type="vegetative mycelia, asexual structures"
/clone_lib="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/note="Vector: pBlueScript SK-; Site_l: EcoRI; Site_2:
Xhol; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into Xhol site of pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gedados.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone INAGE:3724131 3', mRNA sequence.
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gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
rerio cDNA
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                            Length 377;
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34;
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/lab host="XL1-blue MRF"
                                                                                                                                                                                                                                                                                                            Score 16;
Pred. No.
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/organism="Danio rerio"
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High quality sequence stop: 435.
Location/Qualifiers
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/db_xref="taxon:7955"
/clone="IMAGE:3724131"
                                                                                                                                                                                                                                                                        72.7%; SCOL.
100.0%; Pre
0;
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double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). CDNAs for BST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster CDNAs, and a single CDNA from each cluster was chosen for sequencing In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 445)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepton,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Glabons,M., Pape,D., Harvey,N., Schurk,R., Watter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Washu Zebrafish EST Project 1998

Unpublished (1998)

Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 35;
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Putative full length read
The vector to vector length is 522
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/db_xref="taxon:7955"
/clone="IMAGE:5386907"
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Location/Qualifiers
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Danio rerio
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Best Local Simi
Matches 16;
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Contact: Stephen L. Johnson
Washington University School of Medicine
#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: abrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI533213 448 bp mRNA linear EST 26-JUL-2002 fr79a06.xl zebrafish adult brain Danio rerio cDNA clone
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zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzf1s Danio
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Catinopterygii, Neopterygii, Teleostel, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
(bases 1 to 448)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Martin, J., Beck, C., Wylie, T., Pinderwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, T., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                         Gaps
              /clone="IMAGE:4966930"
/sex="mixed male and female"
/tissue type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/note="Vector: pZIPLOX; Site_1: Not!; Site_2: Sall;
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                                                                                                                                                                                                                                                                                                      0; Indels
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High quality sequence stop: 408.
Location/Qualifiers
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/db_xref="taxon:7955"
'tissue_type="brain"
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100.0%; Pred
0; M
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Danio rerio
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Length 452;

12;

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mRNA sequence.
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                        Query Match
Best Local S
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                             MANO2203 452 bp mRNA linear EST 26-JUL-2002 fv14d10.x1 zebrafish adult brain Danio rerio cDNA clone IMAGE:5386435 3', mRNA sequence.
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0
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gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
rerio cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Zbrafishwatson.wustl.edu

CDNA Library Preparation: John Ngai. cDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

Miscorri (web address: www.resqen.com) (email contact:

(web address: www.resqen.com) (email contact:

(web address: www.resqen.com) (email contact:

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (Dases 1 to 452)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyller,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="mixed male and female"
/tissue type="brain"
/dev stage="brain"
/dev stage="radult"
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/clone lib-rary was constructed in lambdaZiPLOX. Mass excision of the cDNA library was performed to yield pzIPLOX plasmids. Insert check was done in original library."
                                                                                                                                                                                    Gaps
Original library was constructed in lambdaZIPLOX. M
excision of the cDNA library was performed to yield
pZIPLOX plasmids. Insert check was done in original
library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Stephen. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                 ;
0
                                                                                                                                      DB 12; Length 448;
                                                                                                                                                                                 Indels
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0
                                                                                                                                 72.7%; Score 16; DB 100.0%; Pred. No. 35; iive 0; Mismatches
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High quality sequence stop: 451.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Danio rerio"
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/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM102203
BM102203.1 GI:17033271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                   181 AAGGCCCGAGAACGTA 166
                                                                                                                                                                                                                             3 AAGGCCCGAGAACGTA 18
                                                                                                                                                            Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                               16;
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
ORGANISM
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BM102203/c
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JOURNAL
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AUTHORS
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FEATURES

ORIGIN

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E I (tases I to 458)

S Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Washu Zebrafish EST Project 1998

Unpublished (1998)

Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: J. 4286 1810
Fax: J. 226 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: zbrafish@watson.wustl.edu
Library constructed by: Bernhard Korn DNA Sequencing by: Washington
University Genome Sequencing Center Clone distribution:
RessourcenZentrumPrimarPatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
rerio cDNA
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                                                                                                                                                                                                                                                                                      1896999 458 bp mRNA linear EST 15-OCT-2001
kS0e03.x1 Zebrafish 15-19hr embryonic cDNA Danio rerio cDNA 3',
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/lab_host="E.Coli (DH10B/KL2blue)"
/clone lib="Zebrafish 15-19hr embryonic cDNA"
/note="Wector: pSPORTI; Site_1: NotI; Site_2: SalI; This Zebrafish library was constructed by Dr. Bernhard Korn (email: b.korn@dkfz-heidelberg.de). RZPD library number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 458)
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Pred. No. 36;
                                                               Indels
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Mismatches
                                                             Mismatches
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Danio rerio"
                  Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:7955"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.7%; Scor.
100.0%; Pre
72.7%; SCUL
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                      BI896999.1 GI:16140135
                                                                                                                                                                                                                                                                                                                                                                                                                                           Danio rerio (zebrafish)
                                                                                                                                               78
                                                                                                               3 AAGGCCCGAGAACGTA 18
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Best Local Similarity 100.
Matches 16; Conservative
                                                                  16; Conservative
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us-09-940-860-3.oligo.rst

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BI708149 452 bp mRNA linear EST 19-SEP-2001 fs42g04.x1 Zebrafish adult olfactory Danio rerio cDNA clone IMAGE:5070534 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            /tiscue type="Olfactory rosettes"
/tab_hose="adult"
/lab_hose="bloth" (dibco BRL)"
/clone lib="zebrafish adult olfactory"
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Zebrafish olfactory epithelium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.7%; Score 16; DB 12; Length 459; 100.0%; Pred. No. 36; 0; Indels cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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High quality sequence stop: 440.
Location/Qualifiers
                                                                      BI708149.1 GI:15683844
                                                                                             Danio, rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 16; Conservative
RESULT 15
BI708149/c
                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                   DEFINITION
                                                                                                                                                         REFERENCE
AUTHORS
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JOURNAL
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Gaps

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Search completed: August 4, 2004, 09:20:54 Job time : 1535.58 secs

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August 4, 2004, 04:00:30 ; Search time 164.337 Seconds (without alignments) 517.009 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                       3373863 segs, 2124099041 residues
                                                                     - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Post-processing: Listing first 45 summaries

geneseqn2001as:* geneseqn2001bs:* geneseqn2003as:* geneseqn2003bs:* N Geneseg 29Jan04:* geneseqn2003cs:* geneseqn2004s:* geneseqn1990s:* geneseqn2000s:* geneseqn1980s:* geneseqn2002s: 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

script		Aaa37797 Helloobac Aaa37796 Helloobac	ın	Aaa37794 Helicobac		Aaa37791 Helicobac	Aav66849 Chlamydia	Aav66846 Chlamydia	Aav66848 Chlamydia	Aav66845 Chlamydia	Aav66850 Chlamydia	Aav66847 Chlamydia	Aas11031 Chlamydia	Aav66851 Chlamydia	Aah28376 Intergeni	Aah28407 Intergeni	Continuation (7 of	Continuation (11 o	Abz34685 Coding se	Aca30087 Prokaryot	Ada69779 Rice gene	Aas46575 Tumour su
H	AAA37798	AAA37796 AAA37796	AAA37795	AAA37794	AAA37793	AAA37791	AAV66849	AAV66846	AAV66848	AAV66845	AAV66850	AAV66847	AAS11031	AAV66851	AAH28376	AAH28407	AAZ01425 06	AAX91990_10	ABZ34685	ACA30087	ADA69779	AAS46575
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ength	1172	1236	1267	1299	1331	1335	1548	1548	1548	1548	1548	1548	1548	1549	2751	2762	110000	110000	1073	1251	3264	5536
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	85.0	80.0	80.0	80.0
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	Abq78796 Nucleotid	Abl71499 Corn tass		Abq78794 Nucleotid	Aal25889 Human bre	Abg78795 Nucleotid	Abq85719 Arabidops	Aal19054 Human bre	Aal08144 Human bre	Aas79337 DNA encod	Aaf67474 Novel hum	Aaf67301 Novel hum	Abv13787 Human pro	Abl81917 Human ova	Aav89330 EST clone	Abv34900 Human pro	Abv43749 Human pro	Adc76303 DNA homol	Adc76983 DNA homol	Abz14572 Arabidops	Aac48695 Arabidops
ABL33832	ABQ78796	ABL71499	ABL76470	ABQ78794	AAL25889	ABQ78795	ABQ85719	AAL19054	AAL08144	AAS79337	AAF67474	AAF67301	ABV13787	ABL81917	AAV89330	ABV34900	ABV43749	ADC76303	ADC76983	ABZ14572	AAC48695
v	9	ø	G	9	4	9	9	4	4	Ŋ	Ŋ	Ŋ	Ŋ	ø	N	Ŋ	rU	σ	თ	9	m
5536	278	281	294	308	348	351	357	358	358	384	390	400	405	405	417	443	443	494	494	525	746
80.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0
16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
24	25	c 26	c 27		29	30	c 31	32	33	34	c 35	36	37	38	39	40	41	c 42	c 43	44	45

ALIGNMENTS

RESULT 1

16SrRNA; detection; strain identification; gastric ulcer; Van Doorn L; Quint W, Helicobacter 16SrRna DNA sequence R28TOTAAL. Haesebrouck F, AAA37798 standard; DNA; 1172 BP. chronic gastritis; zoonoses; ss. Candidatus Helicobacter bovis. 99EP-00870035. 99EP-00870035. De Groote D, (first entry) (revised) WPI; 2000-559879/52. (UYGE-) UNIV GENT. Helicobacter; Ducatelle R, EP1035219-A1, 25-FEB-1999; 25-FEB-1999; 15-SEP-2003 15-JAN-2001 13-SEP-2000 AAA37798; AAA37798

Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes primers for detecting and/or typing Helicobacter strains present in a biological sample.

Claim 2; Page 24-25; 132pp; English.

This sequence represents a Helicobacter 16STRNA sequence of the invention. A probe which specifically hybridises to the 16STRNA sequence and a primer which specifically maplifies it are used for detecting and/or typing Helicobacter Strains present in a biological sample (botained from mammals preferably cattle and pigs) by hybridishing or specifically amplifying the 16S TRNA gene target region of Helicobacter strains present in the biological sample with the primer or probe, strains present in the sological sample with the primer or probe, respectively. The 16S TRNA sequence is also used as a medicament. The 16S TRNA sequence is also used as a medicament. The 16S TRNA sequence is also used as a medicament the 16S TRNA sequences are used for studying and detecting pathogenic

1035 GGAGGAAGGCGAGGATGACG 1054

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a Helicobacter 16SrRNA sequence of the invention. A probe which specifically hybridises to the 16SrRNA sequence and a primer which specifically amplifies it are used for detecting and/or typing Helicobacter strains present in a biological sample (obtained from mammals preferably cattle and pigs) by hybridising or specifically amplifying the 16S rRNA gene target region of Helicobacter strains present in the biological sample with the primer or probe, respectively. The 16S rRNA sequence is also used as a medicament. The 16S rRNA sequence is also used as a medicament. The 16S Helicobacter strains which cause gastric ulcers and chronic gastritis in mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes primers for detecting and/or typing Helicobacter strains present in a
                                                                                                                                             Gaps
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                                                                                                                                           .
0
                                                                                                     Query Match
100.0%; Score 20; DB 3; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                        G; 245 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1194 BP; 327 A; 263 C; 356 G; 248 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quint W,
                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter 16SrRna DNA sequence R27TOTAAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Groote D, Haesebrouck F,
                                                                          Sequence 1172 BP; 323 A; 259 C; 345
                                                                                                                                                                                                   GGAGGAAGGCGAGGATGACG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 24; 132pp; English.
                                                                                                                                                                               1 GGAGGAAGGCGAGGATGACG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candidatus Helicobacter bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-00870035.
                                                                                                                                                                                                                                                                                                   AAA37797 standard; DNA; 1194
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                                                                                                                                                                                                                                                                                                                                                                      (revised)
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biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-1999;
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15-JAN-2001
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                                                                                                                                                                                                                                                                                   RESULT 2
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invention. A probe which specifically hybridises to the 16SrRNA sequence and a primer which specifically amplifies it are used for detecting and/or typing Helicobacter strains present in a blological sample (obtained from mammals preferably cattle and pigs) by hybridising or specifically amplifying the 16S rRNA gene target region of Helicobacter strains present in the blological sample with the primer or probe, respectively. The 16S rRNA sequence is also used as a medicament. The 16S rRNA sequences are used for studying and detecting patchogenic Helicobacter strains which cause gastric ulcers and chronic gastritis in mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                       Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes primers for detecting and/or typing Helicobacter strains present in a
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100.0%; Score 20; DB 3; Length 1236;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1236 BP; 336 A; 271 C; 369 G; 259 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                 Quint W,
                                                                                                                                          Helicobacter 16SrRna DNA sequence R13D001INV.
                                                                                                                                                                                                                                                                                                                                                                                                                 Haesebrouck F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 23-24; 132pp; English
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                                                                                                                                                                                       chronic gastritis; zoonoses; ss.
                                                                                                                                                                                                                         Candidatus Helicobacter bovis.
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                                AAA37796 standard; DNA; 1236
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(first entry)
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                                                                                              (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biological sample.
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                                                                                           15-SEP-2003
15-JAN-2001
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15-JAN-2001
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RESULT 3
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Gaps

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100.0%; Score 20; DB 3; Length 1194;-llarity 100.0%; Pred. No. 0.34; Conservative 0; Mismatches 0; Indels 0

Query Match Best Local Similarity

Matches

1 GGAGGAAGGCGAGGATGACG 20

25-FEB-1999;

EP1035219-A1

13-SEP-2000

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This sequence represents a Helicobacter 16SrRNA sequence of the invention. A probe which specifically hybridises to the 16SrRNA sequence and a primer which specifically maplifies it are used for detecting and/or typing Helicobacter strains present in a biological sample (obtained from mammals preferably cattle and pigs) by hybridising or specifically amplifying the 16S rRNA gene target region of Helicobacter strains present in the biological sample with the primer or probe respectively. The 16S rRNA sequence is also used as a medicament. The 16S rRNA sequence is also used as a medicament. The 16S rRNA sequence is also used as an edicament. The 16S rRNA sequence is also used as an edicament, the 16S rRNA sequence is also used as an edicament, or an entity and detecting pathogenic mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
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                                                                                                                                                                                                                                                                                            Novel isolated 168 rDNA Helicobacter polynucleotides useful as probes or primers for detecting and/or typing Helicobacter strains present in a biological sample.
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                                                                                                                                                               Van Doorn L;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 22-23; 132pp; English.
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                                                                                                                                                               Ducatelle R, De Groote D,
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(first entry)
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les 20; Conserv
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                                  25-FEB-1999;
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15-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention. A probe which specifically hybridises to the 168rRNA sequence and a primer which specifically amplifies it are used for detecting and/or typing Helicobacter strains present in a biological sample (obtained from mammals preferably cattle and pigs) by hybridising or specifically amplifying the 168 rRNA gene target region of Helicobacter strains present in the biological sample with the primer or probe, respectively. The 168 rRNA sequence is also used as a medicament. The 168 rRNA sequence is also used as a medicament. The 168 Helicobacter strains which cause gastric ulcers and chronic gastritis in mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SBP-2003 to standardise
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                                                           Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
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Helicobacter 16SrRna DNA seguence R6XA001.
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                                    This sequence represents a Helicobacter 168rRNA sequence of the invention. A probe which specifically hybridises to the 168rRNA sequence and a primer which specifically amplifies it are used for detecting and/or typing Helicobacter strains present in a biological sample (obtained from mammals preferably cattle and pigs) by hybridising or specifically amplifying the 168 rRNA gene target region of Helicobacter strains present in the biological sample with the primer or probe respectively. The 168 rRNA sequence is also used as a medicament. The 168 rRNA sequence is also used as a medicament. The 168 rRNA sequence is also used as a medicament. The 168 Helicobacter strains which cause gastric ulcers and chronic gastritis in mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
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                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                   Mismatches
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               Claim 2; Page 22; 132pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candidatus Helicobacter bovis.
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(first entry)
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Best Local Similarity
Matches 20; Conserv
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biological sample.
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Helicobacter strains which cause gastric ulcers and chronic gastritis in mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SBP-2003 to standardise OS field)
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the nucleic acid amplification detection of Chlamydia species.
                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                Sequence 1335 BP; 364 A; 294 C; 393 G; 284 T; 0 U; 0 Other;
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(TOKU ) TOKUYAMA SODA KK.
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20; Conserv
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06-JAN-1999
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Best Local S:
Matches 20,
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ID AAV6
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AC AAV6
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28-MAR-1997;

28-MAR-1997;

JP10262679-A.

06-0CT-1998

17-0CT-2003 06-JAN-1999

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The present sequence represents a gene coding Chlamydia 16s ribosome RNA from Chlamydia psittaci. Also described in the present invention are: (1) a recombinant vector containing the above gene; and (2) a transformant transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e. detection of PCR products. (Updated on 17-OCT-2003 to standardise OS field)
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                                   Chlamydia species ribosome genes, and primers derived from it - used for the nucleic acid amplification detection of Chlamydia species.
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the nucleic acid amplification detection of Chlamydia species.
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                                                                                                                                                                                                                                                                                                                 Sequence 1548 BP; 410 A; 328 C; 452 G; 358 T; 0 U; 0 Other;
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                                                                                                  Claim 1; Page 14-15; 18pp; Japanese.
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(TOKU ) TOKUYAMA SODA
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WPI; 1998-587294/50.
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Best Local Similarity
Matches 20; Conserv
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06-JAN-1999
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                                                                                                                           Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
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                                                                                   Chlamydia 16S ribosome RNA gene #2.
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(TOKU ) TOKUYAMA SODA KK.
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(TOKU ) TOKUYAMA SODA KK.
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Best Local Similarity
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28-MAR-1997; 28-MAR-1997;

JP10262679-A 06-OCT-1998.

17-OCT-2003 06-JAN-1999

AAV66848;

RESULT 10 AAV66848

Best Loc Matches

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used for

GGAGGAAGGCGAGGATGACG 1197

1178

AAV66850 standard; DNA; 1548 BP

GGAGGAAGGCGAGGATGACG 20

ð 셤 Chlamydia 16S ribosome RNA gene #6

Chlamydia trachomatis

JP10262679-A

(first entry)

06-JAN-1999

AAV66850;

97JP-00078591. 97JP-00078591

(ATAT-) A & T KK. (TOKU) TOKUYAMA SODA KK.

28-MAR-1997; 28-MAR-1997;

WPI; 1998-587294/50.

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The present sequence represents a gene coding Chlamydia 16s ribosome RNA area Campaida psiteaci. Also described in the present invention are: (1) a recombinant vector containing the above gene; and (2) a transformant transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e. detection of PCR products. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense, bacterial 16s ribosomal RNA, rRNA, bacterial infection, human, food grain supplement, livestock; poultry, therapeutic, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial compound, useful for treating bacterial infections and as livestock and poultry food supplement, comprises antisense oligonucleotides complementary to bacterial 16S and 23S rRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS11021-AAS11034 represent the coding sequences of bacterial 16s ribosomal RNA (rRNA) genes. The sequences were used to design anti-
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the nucleic acid amplification detection of Chlamydia species.
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                                    97JP-00078591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
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                                                                                                          (ATAT-) A & T KK.
(TOKU ) TOKUYAMA SODA KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                   WPI; 1998-587294/50.
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Best Local Similarity
Matches 20, Conserv
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                                    28-MAR-1997;
                                                                        28-MAR-1997;
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24-OCT-2001
06-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a gene coding Chlamydia 16s ribosome RNA from Chlamydia trachomatis. Also described in the present invention are:
(1) a recombinant vector containing the above gene; and (2) a transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e. detection of PCR products

    used for

                                                                                                                                                                                                                                                                                 Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1548 BP; 402 A; 326 C; 470 G; 350 T; 0 U; 0 Other;
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Claim 1; Page 16; 18pp; Japanese.

GGAGGAAGGCGAGGATGACG 1198

1179

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RESULT 13

AAV66847 standard; DNA; 1548 BP

1 GGAGGAAGGCGAGGATGACG 20

Ouery Match
Best Local Similarity 100.0
These 20; Conservative

Chlamydia 168 ribosome RNA gene #3.

Chlamydophila caviae

JP10262679-A

(revised)
(first entry)

17-OCT-2003 06-JAN-1999

AAV66847;

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Gaps

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oligomers containing 8-40 nucleotide subunits, including a targeting nucleic acid sequence at least 10 nucleotides in length which is nucleic acid sequence at least 10 nucleotides in length which is complementary to a bacterial 168 or 235 FWAM nucleic acid sequence. The antisense oligomers are used for treating a bacterial infection in a human or a mammalian animal produced by Escherichia coli, Salmonella typhimurium, Pseudomonas aeruginosa, Vibrio cholera, Neisseria gonorrhoea, Helicobacter pylori, Bartonella henselae, Haemophilus influenza, Shigella dysenterae, Staphylococcus aureus, Mycobacterium tuberculosis, Streptococcus pneumoniae, Freponema palladium and Chlamydia trachomatis. The antibacterial compound may be used as a food grain seuplement in livestock and poultry food composition. Note: The present sequence is not shown in the specification but has been accessed from Genbank using the appropriate accession number given in the specification. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a gene coding Chlamydia 16s ribosome RNA from Chlamydia trachomatis. Also described in the present invention are: (1) a recombinant vector containing the above gene; and (2) a transformant transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia species ribosome genes, and primers derived from it - used for the nucleic acid amplification detection of Chlamydia species.
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  bacterial compounds comprising substantially uncharged antisense
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia 16S ribosome RNA gene #7.
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(TOKU ) TOKUYAMA SODA KK.
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ID AAV6
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Gaps

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Query Match
100.0%; Score 20; DB 2; Length 1549;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0

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1179 GGAGGAAGGCGAGGATGACG 1198
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A1903386 RC-BT029-
A1903431 RC-BT029-
A1903432 RC-BT029-
BF742715 KX34602.Y
BF810332 RC-BT029-
BF810332 RC-BT029-
BG875496 PM3-BT065
BF810203 RC6-CT000
BG876496 PM3-BT065
BF810203 RC6-CT000
BG987045 PM0-HT116
BF810198 RCF-CT000
CD05765 PM1-BT16
BF810198 RCF-CT000
CD164371 ML1-00877
BF81049 BCC-CT000
CD164371 ML1-00877
BF819649 BACPP13-M
BF910944 CM1-UT003
BG352721 WR1-HT085
AW804622 CW1-UM009
BC37466 BM3-BN006
BH35798 BACPP13-M
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CD091064 MC1-C004U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 122)

Dias Neto,E., Garrea,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., G.Y., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
AW947763 RCO-MT000
CD164995 ML1-0093T
H74424 126 Standar
AT000468 AT000468
BH831104 BACP92-L
CF33898 RCLI--03-
BX000722 BX000722
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BH831257 BACPP33-C
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RC-BI029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence.
                                                                                                                    BG874702 CM0-BN007
BG874706 CM3-BN007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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BG9745
A1903306
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CD097562
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                    - nucleic search, using sw model
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                    Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT029-113_1.html&t3=100199&t4=1)
                                                                                                                                                                                                                                                                                     /dev_stage="Adult" / clone_lb="BT029" / clone_lb="BT029" / clone_lb="BT029" / clone_lb="BT029" / clone_lb="BT029" / clone_rb="Organ: breast; Vector: puc18; Site_1: A min!-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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PM3-BT0654-030300-002-d12 BT0654 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 9; Length 122; 100.0%; Pred. No. 0.078; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/sex="female"
                                                                                                                                                            Seq primer: puc 18 forward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCAAACAGGATTAGATACCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 GCAAACAGGATTAGATACCC 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Best Local
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VERSION
KEYWORDS
SOURCE
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PUBMED
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BE084285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                     FEATURES
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CD088408 174 bp mRNA linear EST 14-SEP-2003 MC1-0050T-R112-C03-U.G MC1-0050 Schistosoma mansoni cDNA clone MC1-0050T-R112-C03.G, mRNA sequence. CD088408
                   /mol_type="mrna" | /mol_type="mrna" | /mol_type="mrna" | /mol_type="mrna" | /mol_type="mrna" | /mol_type="mrna" | /moles"/organ: profes | /moles"/organ: progras; vector: pucl8; site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 16,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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1 (bases 1 to 188)
Wang, Y., Yang, C., Jiang, J., Liu, G., Wu, J. and Liu, Z.
EST aquired from cDNA library of Tamarix androssowii treated with NaHCO3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF199424 linear EST 01-AUG-2
EST1023 Tamarix androssowii leaf Tamarix androssowii CDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Northeast Forestry University
Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
Tel: 086-451-219060.
Email: WANGYUCHENG1029@YAHOO.COM.CN.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .168
/organism="Tamarix androssowii"
/mol type="mRNN"
/db xref="taxon:189785"
/tissue type="leaf"
/clone_lib="Tamarix androssowii leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB 14;
100.0%; Pred. No. 0.081;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yucheng Wang
Forestry Source and Environment College
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                       stringency conditions."
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Eukaryotes, Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases I to 203)

1 (bases I to 203)

1 (bases I to 202)

2 (bases I to 202)

3 (bases I to 202)

3 (bases I to 202)

4 (b
                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
Bmail: asimpsom@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCO-MT0006-110
300-021-dl0&t3=2000-03-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence start: 20
High quality sequence story: 186.
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ML1-0093T-D139-B11-U.G ML1-0093 Schistosoma mansoni cDNA clone
ML1-0093T-D139-B11.G, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone lib="MT0006"
/note="Corgan: marrow; Vector: puc18; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No: 16,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA, and cDNA amplification were performed under low
                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
sequencing of the human transcriptome with ORF expressed
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                                            sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202653
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Departamento de Bioquimica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genet. 35 (2), 148-157 (2003)
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Schistosoma mansoni
                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
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Matches 20; Conserv
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CD164995
LOCUS
DEFINITION
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MEDLINE
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                                                                                                                                              Homo sapiens (human)
Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Correa, Catarrhini, Hominidae, Homo.

(bases 1 to 186)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Fax: +55-11-3081-3186

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimia - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="cercaria"
|Jab host="Biomphalaria glabrata"
|clone lib="MCI-0050"
|note="Vector: pGEM T-easy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .174
/organism="Schistosoma mansoni"
/or_Lype="mRNA"
/db xref="taxon:6183"
/clone="MC1-0050T-R112-C03.G"
/sex="mixed pool"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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22879926
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EST.
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                                                                                     Schistosoma mansoni
Schistosoma mansoni
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BH831104.1 GI:21028448
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                                                                                                                                       Similarity
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Best Local S:
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AT000468/c
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Matches
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Brassica napus

Wararyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I bases I to 214)
Park, Y.S., Kwak, J.M., Kwon, O.Y., Kim, Y.S., Lee, D.S., Cho, M.J.,
Lee, H.H. and Nam, H.G.
                                                                         Fax: +55-11-3031-2186
Email: verjo@qusp.br
Email: verjo@qusp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Location/Qualifiers
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Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
Brasil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Molecular Genetics Laboratory
Pohang University of Science and Technology
Dept. of Life Science, San31 Hyojadong, Pohang Kyungbuk 790-784,
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126 Standard Brassica napus cDNA clone R185F, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 205;
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                                                                                                                                                                                                                                                          /organism="Schistosoma mansoni"
                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:6183"
/clone="ML1-0093T-D139-B11.G"
                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pGEM T-easy"
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                                                                                                                                                                                                                                                                                                                                      /sex="mixed pool"
/dev_stage="miracidium"
/clone_lib="ML1-0093"
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Fax: 825622792199
Email: nam@vision.postech.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="L. cv Naehan"
/db_xref="taxon:3708"
/clone="R185F"
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                                                              Tel: +55-11-3091-2173
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H74424
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (Bases II to 221)
1 (Bases II to 221)
Bvaluation of 515 expressed sequence tags obtained from guard cells of Brassica campestris
Planta 202 (I), 9-17 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AT000468 Brassica rapa guard cell Brassica rapa subsp. pekinensis cDNA clone DGT85, mRNA sequence.
AT000468.1 GI:3414002
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BACPP32-L04.z Pristionchus pacificus BAC ends Pristionchus
pacificus genomic, genomic survey sequence.
BH831104
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     as
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Contact: Hong-Gil Nam
Department of Life Science, Plant Molecular Genetics Laboratory
Pobnan University of Science and Technology
San 31 Hyojadong, Pohang Kyungbuk 790-784, Korea
Email: hgn@bric.postech.ac.kr
Submitted through BRIC(Biological Research Information Center) of
Korea URL: http://pinc.postech.ac.kr/.
Location/Qualifiers
with Pharmacia's cDNA synthesis kit using oligo(dT) a primer. The Eco RI/Not I adaptor was ligated to the dSDNA. The cDNAs inserts were cloned into the pUC19 vector digested with EcoRI."
                                                                                                                                                                                                                 Gaps
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Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
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0
                                                                                                                                                              14; Length 214;

    .221
    /organism="Brassica rapa subsp. pekinensis"

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/clone_lib="Brassica rapa_guard_cell"
                                                                                                                                  100.0%; Score 20; DB 14, ilarity 100.0%; Pred. No. 0.083; Conservative 0; Micmet-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="DGT85"
                                                                                                                                                                                                                                                                                                124 GCAAACAGGATTAGATACCC 143
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Gaps ;

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/tissue type="xylem"
/close lib="pins" |
/close lib="formuse pinseter xylem"
/note="Compression wood was induced in four 14-year old
maritime pine clones by artifitial bending. Control clone
(no bending) were sampled for xylem associated with early
wood and late wood at the beginning (April) and at the end
(August) of the growing seasons. Differentiating xylem
corresponding to Early wood, late wood, compression wood
and opposite wood were used for mRNA fingerprinting using
the cDNA-APIPP assay."
                                                                                                                                                                                                                                                                                                                                                 BX000722 Finus pinaster xylem Pinus pinaster CDNA clone PPEM56, mRNA sequence.
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CMO-BN0075-220200-237-h05 BN0075 Homo sapiens cDNA, mRNA sequence.
BG874702
BG874702.1 GI:14251633
EST.
end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pinus pinaster
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pin
1 (bases 1 to 275)
Le Provost, G., Paiva, J., Pot, D., Brach, J. and Plomion, P.
Seasonal variation in transcript accumulation in wood forming
tissue of maritime pine (Pinus pinaster Ait.) with emphasis on
cell wall Glycine Rich Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 13; Length 275; 100.0%; Pred. No. 0.085;
                                                                                                      Length 248;
                                                                                                                                                  0; Indels
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Email: Frigerio@pierroton.inra.fr.
Location/Qualifiers
                                                                                                      Score 20; DB 14;
Pred. No. 0.084;
Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="PPEM56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Frigerio JM
Genetique et Amelioration 69
                                         regenerated media'
                                                                                                                                                                                                                                           159 GCAAACAGGATTAGATACCC 178
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1 Similarity 100.0%; P:
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sapiens
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AUTHORS
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FCL1--03-G23.gl Regenerated callus lambda phage cDNA library (RCL1)
Cryza sativa cDNA clone RCL1--03-G23, mRNA sequence.
CF338988
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
1 (bases 1 to 248)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, Myongdi University
Yongin, Kyeongi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                1 (bases I to 243)
Srinivasan, J., Sinz, W., Lanz, C., Bránd, A., Nandakumar, R.,
Raddatz, G., Witte, H., Keller, H., Kipping, I., Pires da Silva, A.,
Jesse, T., Millare, J., de Both, M., Schuster, S.C. and Sommer, R.J.
A BAC-based genetic linkage map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA" |
|strain="var. California"
|db xref="taxon:54126"
|clone_lib="Pristionchus pacificus BAC ends"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 28; Length 243; 100.0%; Pred. No. 0.084; ive 0; Mismatches 0; Indels
                                                                                                                                           Unpublished (2002)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601372
Email: ralf: sommer@tuebingen.mpg.de
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/mol_type="mRNA"
cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCLL"-03-G23"
/tissue_type="callus"
  Neodiplogasteridae; Pristionchus.
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Matches 20, Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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/mol_type="mRNA"
/do_type="mRNA"
/do_type="mRNA"
/do_type="mRNA"
/dov_stage="Adult"
/clone_lib="BN0075"
/note="Organ: breast normal; Vector: pucl8; Site_1: Smal;
/note="Organ: breast normal; Smal;
/note="Organ: breast normal; Smal;
/note="Organ: breast normal; Smal; Smal;
/note="Organ: breast normal; Smal; Smal;
/note="Organ: breast normal; Smal; Smal
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases I to 297) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Eriones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., Olymare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Tel: +55-11-2704922
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-BN0075-220 200-237-h05&t3=2000-02-22&t4=1)
High quality sequence stop: 297.
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1 (Dases 1 to 301)
Dias Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., Costán,S., Costán,F., Briva,W.Jr., Sago,M.A., Bordin,S., Costán,F., Brunstein,A., Garvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                    Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed shotgun sequencing
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Fax: +55-11-2707001
Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM3-BN0075-240
200-101-h05&t3=2000-02-24&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence start: 19
High quality sequence story: 301.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                     Sao Paulo-SP,
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RC-BT029-070199-018 BT029 Homo sapiens cDNA, mRNA sequence.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Matches
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT029-018.html
&t3=070199&t4=1)
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1 (bases 1 to 312)
Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Harck,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev stange="Adult"
/clone lib="BT029"
/clone lib="
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT029-165.html &t3=110199&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Eug Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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RC-BT029-110199-165 BT029 Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
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Location/Qualifiers
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                                                                      /clone_lib="BT029"

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//clone=logan: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES FOR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                  stringency conditions.
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Job time: 1397.25 secs
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Title: Perfect

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Gaps

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Query Match 100.0%; Score 20; DB 39; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 20; Conservative 0; Mismatches 0;

1 GCAAACAGGATTAGATACCC 20 GCAAACAGGATTAGATACCC 20

Length 20; Indels

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; OTHER INFORMATION: synthetic amplification primer US-09-940-860-1
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US-110-343-319-77
US-110-343-319-80
US-110-343-319-80
US-110-343-319-82
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US-10-343-319-102
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US-09-283-655-1
US-09-620-375-1
US-10-715-220-1
US-09-940-860-6
US-08-246-935-2
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US-10-343-319-88
US-10-343-319-89
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US-10-343-319-91
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GENERAL INFORMATION:
APPLICANT: Nothman, Richard
APPLICANT: Nothman, Radard
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BAC
FILE REFERENCE: 01107.00185
CURRENT PEPLICATION NUMBER: US/09/940,860
CURRENT FILING DATE: 2001-08-29
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SECOID NO.
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ORGANISM: Artificial Sequence
FEATURE:
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Match 1
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US-09-940-860-1
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TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH

TITLE OF INVENTION: CHRONIC FAIIGUE SYNDROME AND RELATED DISORDERS

TITLE OF INVENTION: CHRONIC FAIIGUE SYNDROME AND RELATED DISORDERS

CURRENT PILING DATE: 108/09/620,375

CURRENT PILING DATE: 2000-07-20

PRIOR PILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PASKSEQ for Windows Version 3.0

LENGTH: 25
                                                                                            APPLICANT: Vojdani, A.
TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS
FILE REPERENCE: IMSCI.009A
CURRENT PELLING NUMBER: US/09/283,655
CURRENT FILING DAIE: 1999-04-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 25
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100.0%; Score 20; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic oligonucleotide primer
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RESULT 2
US-09-283-655-1
; Sequence 1, Application US/09283655
; GENERAL INFORMATION:
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US-09-620-375-1
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Best Local Similarity
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LENGTH: 50
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GENERAL INFORMATION:
APPLICANT: Weisburg, William G.
APPLICANT: Lane, David G.
APPLICANT: Lane, David G.
TITLE OF INVENTION: A METHOD FOR DETECTING AND IDENTIFYING
TITLE OF INVENTION: PATHOGENIC ORGANISMS USING TARGET SEQUENCES AS DETECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                         APPLICANT: Vojdani, A.

TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: CHECOLIC FAITGUE SYNDROME AND RELATED DISORDERS
FILE REPERENCE: IMSCI.009A
CURRENT APPLICATION NUMBER: US/10/715,220
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US/09/283,655
PRIOR FILING DATE: 1999-04-01
SPRIOR FILING DATE: 1999-04-01
SPRIOR FILING DATE: 1999-04-01
SUMBER OF SEQ ID NOS: 8
SOFTWARE: FASESQ for Windows Version 3.0
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100.0%; Score 20; DB 39; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
GENERAL SETTLE OF INVENTION:
GURRENT FILING DATE:
GURRENT FILING DATE:
GURRENT FILING DATE:
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic oligonucleotide primer US-10-715-220-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: synthetic amplification primer US-09-940-860-6
                                 Sequence 1, Application US/10715220 GENERAL INFORMATION:
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US-08-246-935-2/c
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GENERAL INFORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Mangala A.
TITLE OF INVENTION: A MITHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: PCT/AU01/00933
FRIOR APPLICATION NUMBER: PCT/AU01/00933
FRIOR APPLICATION NUMBER: AU PQ9090/2000
FRIOR FILING DATE: 2001-07-27
FRIOR PLEICATION NUMBER: AU PQ9090/2000
FRIOR FILING DATE: 2000-07-28
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                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,935
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Pred. No. 0.14;
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; CTHER INFORMATION: Helicobacter pylori also.
US-10-343-319-76
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Best Local Similarity 100.0%; Pred. No. (
Matches 20; Conservative 0; Mismatche
                                                                                                                                                                            FILING DATE:
FILING DATE:
CLASSIFICATION: 435
FRIOR APPLICATION NUMBER: US 07/707,646
FILING DATE: 30-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: GTR90-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)861-6240
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
ZIP: 02173
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: GTS OLIGO NUMBER 1739
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                                                                                                                GENERAL INFORMATION:

APPLICANT: HURLEY, Neil

APPLICANT: Harder, Neil

APPLICANT: Martin, Fjelda E.

APPLICANT: Martin, Fjelda E.

APPLICANT: Martin, Fjelda E.

ITILE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS

TILE REFERENCE: DAVI139.002APC

CURRENT PAPLICATION NUMBER: US/10/343,319

CURRENT PILING DATE: 2003-09-17

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 106

CENTRARE: PRACEEQ FOR WINDOWS VERSION 4.0
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APPLICANT: Huncer, Neil
APPLICANT: Huncer, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002APC
CURRENT FILING DATE: 2003-09-17
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US/10/343,319
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SEQ ID NOS 106
SEQ ID NOS: 106
SEQ 
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has 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ; ORGANISM: Thiomicrospira denitrificans US-10-343-319-80
                                                    Sequence 80, Application US/10343319 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-343-319-81
; Sequence 81, Application US/10343319
; GENERAL INFORMATION:
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; ORGANISM: Neisseria meningitidis
US-10-343-319-81
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hes 20; Conserva
                          US-10-343-319-80
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Pred. No. 0.14;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             Sequence 77, Application US/10343319
GENERAL INFORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Hunter, Neil
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI339,002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR PLILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: AU PQ9090/2000
PRIOR PLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SCO ID NO 77
SEQ ID NO 77
SEQ ID NO 77
LENGTH: 50
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APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
TITLE OF INVENTION: A METHOD OF DETECTING MICROCRGANISMS
FILE REFERENCE: DAVI139 OGAPC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT APPLICATION NUMBER: PCT/AU01/00933
PRIOR APLICATION NUMBER: PCT/AU01/00933
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SEQ ID NO 79
LENGTH: 50
0; Indels
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 20; Conservative 0; Mismatches
0; Mismatches
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US-10-343-319-77
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CRGANISM: Leptothrix mobilis
US-10-343-319-79
20; Conservative
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Best Local Similarity
Matches 20; Conserv
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NAME/KEY: misc_feature
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Best Local Similarity
Matches 20; Conserv
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US-10-343-319-85
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GENERAL INFORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Hunter, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
TITLE OF INVENTION: A METHOD OF DETECTING MICRORGANISMS
FILE REFERENCE: DAVI139,002APC
CURRENT APPLICATION NUMBER: RCT/AU01/00933
PRIOR FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: RCT/AU01/00933
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: AU PQ9090/2000
PRIOR APPLICATION NUMBER: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 83
LENGTH: 50
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT PILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/AŬ01/00933
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2000-07-27
PRIOR PILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOTTWARE: FRSESEQ for Windows Version 4.0
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APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda B.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
PRIOR APPLICATION NUMBER: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR PILING DATE: 2001-07-27
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                            SEQ ID NO 82
LENGTH: 50
TYPE: DNA
ORGANISM: Actinobacillus actinomycetemcomitans
US-10-343-319-82
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OTHER INFORMATION: Also Vibrio cholerae, Pseudomonas aeruginosa, and OTHER INFORMATION: Rhodospirillum rubrum.
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                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: AU PO9090/2000
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84
LENGTH: 50
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Job time : 1826.78 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Salmonella typhi
                                                                                              ; TYPE: DNA; ORGANISM: Escherichia coli
US-10-343-319-84
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Perfect score:

Title:

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Sequence:

Scoring table:

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Searched:

Database :

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Mus musculus (house mouse)

Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musculus

I (bases I to 304)

Scono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,

Fukuda, S., Fukunishi, Y., Hara, A., Hayateu, M., Hirozane, T., Hori, F.,

Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,

Kai, C., Kawai, J., Kikuchi, N., Kojan, S., Kusakabe, M.,

Matsuyama, T., Miki, R., Mizuo, Y., Nakamura, M., Oda, H., Okazaki, Y.,

Shibatea, Y., Saito, H., Sano, M., Sato, K., Shibata, Y.,

Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N.,

Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,

Tokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,

Riken Mouse Ests (Konno, H., et al. 1999)

Li Onpublished (1999)
           CA199884 SCRIFTION
CA199884 SCRIFTION
CC6236557 SCSBFL501
CC653693 GANBBD029
CG734728 ZMBBD029
CG734728 ZMBBD029
CG73893 PUFLB28TD
CG03893 PUFLB29TD
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A1941805 618035E02
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CC771463
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                               RESULT 1
AV295422
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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CG093861 PUFSX26TB
                                                                                                       August 4, 2004, 05:41:25; Search time 1393.25 Seconds (without alignments) 428.668 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                              55026578
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                       27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                         OM nucleic - nucleic search, using sw model
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BG380134
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TITLE
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RHIZ2 23 H01.b1 A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
sequence.
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//ab_host="NH10B"
//clone_lib="Riter | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 131-1 | 13
                                                                                                                                                                                                                                                                                                                                                                                  Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M. Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Okazaki, Y. Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Ozawa, Y., Muramatsu, M., Attomated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                Email: genome-res@gsc.riken.go.jp,
URi.http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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clone="5730434H04"
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/strain="C57BL/6J"
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BG102240.1 GI:12617185
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100.0%;
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                                                                                                                                                      Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum propinguum
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Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
776: 319 335 956
Fax: 319 335 966
Fax: 319 335 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum propinguum"
/mol type="mRNA"
/db_xref="taxon:132711"
/clone lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site_1: Khoi, Site_2: EcoRi; The library was made Erom poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                 Pratt, L.H.
An EST database from Sorghum: Sorghum propinguum rhizomes Unpublished (2000)
Unpublished (2000)
Laborat: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fat: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                      Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
Seg primer: JEN REV
High quality sequence stop: 377
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(Dases 1 to 567)

Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
         /clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pcR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:4577"
/clone="xxmara0725604"

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9712 Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Center Drive, Rockville, MD 20850, USA
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                   Length 530
                                                                                                                                                                                                                           0; Indels
                                                                                                                                                             Query Match 90.0%; Score 18; DB 29; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0;
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/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Zea mays"
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Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFSX26TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                             117 GGAGGAAGGCGAGGATGA 134
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Saccharum officinarum
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Class: sheared ends.
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CA199884/c
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                                                                                                                                                                                                                                                                     /bx.ref="texaon:1016"
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polylinker; Site 1: Not 1; Site 2: Bco RI; The UI-R-CSO
library is a normalized library constructed from the
following rat heart tissues: embryonic day 17, embryonic
day 19, embryonic day 21, adult day 1, adult day 12, adult
day 75, adult day 200. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest.eng.ulowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG_IIS-UI-R-CSO
TAG_LIB-UI-R-CSO
TAG_LIB-UI-R-CSO
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PUFSX26TB ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa0725F04,
CG093861
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90.0%; Score 18; DB 12; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Fax: 301-838-0208
Email: whitelaw@tigr.org
elements were found in this cDNA sequence: 1-23, >AT rich#Low complexity
Seq princh : M13 Forward
POLYATYES.
                                                                                                                                                                   1. .508
/organism="Rattus norvegicus"
                                                                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                                               Location/Qualifiers
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Class: sheared ends.
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Contact: Cathy Whitelaw
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/ Organism="Saccharum officinarum"
/mol_type="mRNA"
/db xref="taxon:4547"
/db xref="taxon:4547"
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Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sixing between 0.8 and 1.5 KD were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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Saccharum officinarum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
                                                                                                                                                                                                Centror de Biología Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1039
Email: paruda@wuicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 013 row: D column: 09
Seq primer: TP Pronocer Primer.
Location/Qualifiers
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
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Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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| 1. .617 |
| Corganism="Casccharum officinarum" |
| Corganism="Casccharum officinarum" |
| Corganism="Cascribio |
| Clone | SCSBPE15014809" |
| Clone | Lib="Casccharum officinarum FLS" |
| Clone | Lib="Casccharum officinarum offic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      784 bp DNA linear GSS 19-JUN-2003
OGJAO16TV ZM 0.7_1.5_KB Zea mays genomic clone ZNMBMa0295D07,
genomic survey sequence.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 784)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
citek, R.W., Nunbarg, A., Robbins, D. and Lakey, N.
Unpublished (2002)
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br Plate: 014 row: E column: 09 Seq primer: 77 Promoter Primer.
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methylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
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Class: sheared ends.
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CC657309.1 GI:32060634
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genomic survēy sēquence.
CG458612
CG458612.1 GI:34843612
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Homo sapiens (human)
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                   Homo sapiens
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Zea mays subsp. mays
Eukaryota; Viridiplante; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnollophyta; Lillopsida; Poales; Poaceae; FACCAD
alade; Panicoideae; Andropogoneae; Zea.

I (bases 1 to 784)
S Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
S Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
S Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
S Yu,Y., Ming,R.
Sequencing of the maize genome
Unpublished (2003)
Arizona Genomics Institute
University of Arizona
Blological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
BS721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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BE743778 BE743778
EB743778
EST.
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             Query Match 90.0%; Score 18; DB 29; Length 784; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 18; Conservative 0; Mismatches 0; Indels
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Plate: 0290 row: C column: 20
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .784
                                                                                                                      484 GGAGGAAGGCGAGGATGA 467
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B 1 (Dases I to see, National Control of Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: gapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

CONA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM755 row: k column: 21

High quality sequence stop: 771.
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(Dases 1 to 867)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Maize Genomics-Consortium
Unpublished (2003)
Other GSSS: PURKS4TE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 826)
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FEATURES

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CG038933 972 bp DNA linear GSS 19-AUG-2003 PUFLB28TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0674F0B, genomic survey sequence. CG038933.1 GI:33911089
951 bp DNA linear GSS 19-AUG-2003 purlb28TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0674F08, CG038934
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 972)
1 (bases 1 to 972)
Resinck, A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resinck, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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1 (bases 1 to 951)
Whitelaw, C.A., Ouackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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CoT selected genomic DNA library"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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19712 Medical Center Drive, Rockville, MD 20850, USA
1971: 301-838-5843
Fax: 301-838-0208
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Unpublished (2003)
Other_GSSs: PUFLB28TD
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Unpublished (2003)
Other GSSs: PUFLB28TB
Contact: Cathy Whitelaw
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Class: sheared ends.
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CoT selected genomic DNA library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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                                                                                                                                                                                                                                                                                                                          ch 90.0%; Score 18; DB 29; Length 867; I Similarity 100.0%; Pred. No. 1.3e+02; 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850, USA 121: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .890
/organism="Zea mays"
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Class: sheared ends.
Location/Qualifiers
                                            Class: sheared ends.
Location/Qualifiers
1. .867
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Unpublished (2003)
Other GSSs: PUFDX67TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  812 GGAGGAAGGCGAGGATGA 795
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source

ORIGIN

FEATURES

RESULT 13 CG038934/c

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RESULT 12 BZ803618/c LOCUS VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

Query Match Best Local

ORIGIN

Matches

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Gaps

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Job time : 1397.25 secs

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BZ803611.1 GI:29012211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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1 (bases 1 to 992)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
Waize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFDX67TD
Contact: Cathy Whitelaw
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Class: sheared ends.
Location/Qualifiers
1. 992
| vorganism="Zea mays" |
| mol_type="genomic DNA" |
| strain="B73" |
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| clone="IxMBTA297Ki4" |
| clone="IxMBTA297Ki4" |
| clone="taxon:4577" |
| clone="taxon:4577
                                                                                                                                  1. .972

/ organism="Zea mays"

/mol_type3"

/mol_type3"

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/db_xref="taxon:457"

/clone="ZMNBTa664F08"

/clone="Lib="ZM 0.6 1.0 KB"

/note="Vector: pcR4-10PO, Site_1: EcoRI; 0.6-1.0 kb high

CoT selected genomic DNA library"
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90.0%; Score 18; DB 28; Length 992;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Seg primer: TR
Class: sheared ends.
Location/Qualifiers
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BZ803611
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AUTHORS
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JOURNAL
COMMENT
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                                                                                               FEATURES
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Search completed: August 4, 2004, 09:20:51

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16, Appl 16, Appl 16, Appl 16, Appl 16, Appl 18, Appl 18, Appl 101, App 102, Appl 62, Appl 62, Appl 64, Appl 65, Appl 65, Appl 64, Appl 65, Appl 67, Appl 67, Appl 67, Appl 67, Appl 67, Appl 68, Appl 68, Appl 69, Appl 61, Appl 61, Appl 62, Appl 62, Appl 63, Appl 64, Appl 65, Appl 65, Appl 66, Appl 67, Appl 67, Appl 68, Appl 68

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RESULT 1
US-10-417-884A-3170/c
US-10-417-884A-3170, Application US/10417884A
is Gequence 3170, Application:
i General INFORMATION:
i GENERAL INFORMATION:
i TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION:
ENTEROCOCCUUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                      Sequence 1
Sequence 1
Sequence 1
Sequence 6
Sequence 1
Sequence 1
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Sequence 1
Sequence 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
US-10-148-328B-85
US-10-148-328B-88
US-10-148-328B-88
US-10-808-807-16
US-10-808-977-16
US-10-804-1398-16
US-10-804-1398-16
US-10-804-1388-16
US-10-804-1388-16
US-10-804-1388-16
US-10-148-328B-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: CL/ACL. CCOMPUTER: CC CORPATING SYSTEM: ACT CORPATING SYSTEM: ACTI CTREAT ASCII CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/417,884A FILING DATE: 17-APT-2003
PRIOR APPLICATION NUMBER: US/09/107,532 FILING DATE: 30-Jun-1998
APPLICATION NUMBER: G0/085,598 FILING DATE: 14 May 1998
APPLICATION NUMBER: G0/051571 FILING DATE: 14 May 1998
APPLICATION NUMBER: G0/051571 FILING DATE: 14 May 1998
APPLICATION NUMBER: G0/051571 ATTORNEY/AGNT INPORMATION: NAME: ATIORAL DENCE DENCE TO TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SED ID NO: 3170:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SED ID NO: 3170:
                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: circular
ULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
   11300
13300
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
   100.0
                                                                                                                                                                                                                                                                                                  100.0
     Sequence 3170, Ap
Sequence 14013, A
Sequence 14013, A
Sequence 74, Appl
Sequence 5, Appl
Sequence 5, Appli
Sequence 100, Appl
Sequence 100, Appl
Sequence 64, Appli
Sequence 64, Appli
Sequence 64, Appli
Sequence 66, Appli
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98, APP1
76, APP1
92, APP
104, APP
60, APP1
95, APP1
95, APP1
                                                                                                                  August 4, 2004, 06:43:54; Search time 199.036 Seconds (without alignments) 247.629 Million cell updates/sec
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9: /cgn2_6/ptodata/2/pna/USO0_NEW COMB.seq:*
9: /cgn2_6/ptodata/2/pna/USO0_NEW COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                     9508132
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-417-884A-3171
US-10-79-479-14013
US-10-148-3288-75
US-10-148-3288-75
US-10-148-3288-75
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US-10-148-328B-95
US-10-148-328B-106
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                                                                                                                                                                                                                                                                                                                 4754066 seqs, 1232178907 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                      using sw model
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Gapop_60.0 , Gapext 60.0
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No.
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 363
; OTHER INPERMATION: s=g or c
US-10-793-479-14013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Unknown organism
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NAME/KEY: modified_base
LOCATION: (494)
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3171, Application US/10417884A
Sequence 3171, Application US/10417884A
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                    100.0%; Score 20; DB 7; Length 279; ilarity 100.0%; Pred. No. 0.021; Conservative 0; Mismatches 0; Indels
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100.0%; Score 20; DB 7; Length 279;
Bewit Local Similarity 100.0%; Pred. No. 0.021;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER:
FILING DATE: 17-2003
PRIOR APPLICATION NUMBER: US/09/107,532
APPLICATION NUMBER: 00/085,598
FILING DATE: 30-30n-1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: 30-30 APPLICATION NUMBER: 50/081571
APPLICATION NUMBER: 50/081571
FILING DATE: 30-30 APPLICATION NUMBER: 50/081571
ATTORNEY/AGENT INFORMATION:
                      NAME/KEY: misc_feature; 10CATION: (B) LOCATION 1...279; SEQUENCE DESCRIPTION: SEQ ID NO: 3170: US-10-417-884A-3170
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LOCATION: (B) LOCATION 1...279
; SEQUENCE DESCRIPTION: SEQ ID NO: 3171:
US-10-417-884A-3171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEFAX: (781)893-8077
INFORMATION FOR SEQ ID NO: 3171:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <UNKNOWN>
                                                                                                                                                                                                                                                   LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER:READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 20; Conservat
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US-10-486-307-5/c
Sequence 5, Application US/10486307
Sequence 5, Application US/10486307
GENERAL INFORMATION:
APPLICANT: E.I. duPont de Nemours, Inc.
TITLE OF INVENTION: GENES ENCODING BARYER-VILLIGER MONOOXYGENASES
FILE REFERENCE: CL1789 PCT
CURRENT APPLICATION NUMBER: US/10/486,307
CURRENT FILLING DATE: 2004-02-05
PRIOR PILLING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Microsoft Office 97
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Pred. No. 0.019;
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 20; Conservative 0; Mismatches
         0; Mismatches
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APPLICANT: JEANNIN, PASCALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 gcadacaddarradaraccc 593
                                                                                                   696 GCAAACAGGATTAGATACCC 677
                                                      1 GCAAACAGGATTAGATACCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; ORGANISM: Brachymonas sp. CHX
US-10-486-307-5
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ORGANISM: Unknown organism
         Conservative
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         20;
         Matches
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GENERAL INFORMATION:
APPLICANT: Rosenberg, Eugene
APPLICANT: Ros, Elicra Z.
APPLICANT: Ron, Elicra Z.
APPLICANT: Ron, Elicra Z.
APPLICANT: Ron, Elicra Z.
APPLICANT: ACID AS THE NITROGEN SOURCE
FILE REFERENCE: 27821
CURRENT APPLICATION NUMBER: PCT/LL04/00351
CURRENT PILING DATE: 2004-04-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DERNONET, JEAN-LUC
APPLICANT: GUERINEAU, MICHEL
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE AREFERENCE: 03806.0547-0000
CURRENT APPLICATION NUMBER: US/10/148,328B
CURRENT FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1299-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-16-07
NUMBER: PELLING DATE: 300-10-07
SOFTWARE PAPELICATION NUMBER: 60/209,800
PRIOR FILING DATE: 2000-06-07
NUMBER: PAPELICATION NUMBER: 60/209,800
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Local Similarity 100.0%; Score 20; DB 8; Length 601;
Local Similarity 100.0%; Pred. No. 0.02;
nes 20; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.019;
; OTHER INFORMATION: variable nucleotide US-10-148-328B-74
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                                                                                                                                                                                                                                                                                                                                      , Application US/10148328B
                                                                                                                                                                                                  265 GCAAACAGGATTAGATACCC 284
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                                                                                                                                                                       1 GCAAACAGGATTAGATACCC 20
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Best Local Similarity
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SEQ ID NO 5
                                                                                                                                                                                                                                                                                                             US-10-148-328B-75
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Matches
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TYPE: DNA
ORGANISM: Unknown organism
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Matches 20; Conservative
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Sequence 100, Application US/10148328B

Sequence 100, Application US/10148328B

Sequence 100, Application US/10148328B

Sequence 100, Application US/10148328B

APPLICANT: DERNODET, JEAN-LUC

APPLICANT: GURRINALW MICHEL

APPLICANT: SIMONET, PASCAL

TITLE OF INVENTION: BATHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT

TITLE OF INVENTION: BATHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT

TITLE OF INVENTION: GAMPIE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS

TITLE OF INVENTION: OF NOVEL COMPOUNDS

TITLE OF INVENTION: OF NOVEL COMPOUNDS

TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS

CURRENT APPLICATION NUMBER: US/10/148,328B

CURRENT FILING DATE: 2002-05-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 126

SOFTWARE: PALENTIN Ver. 3.2

SEQ ID NO 100

LENGTH. 1197
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US-10-148-328B-81

i Sequence 11 Application US/10148328B

j GENERAL INFORMATION:

APPLICANT: DEANNIN, PASCALE

APPLICANT: DEANNIN, PASCALE

APPLICANT: GURRINEAU, MICHEL

APPLICANT: SIMONET, DEANNINO, DEANNION BAPLICANT: TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS FROM AN ENVIRONMENT

TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS

TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS

TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS

TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS

TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS

CURRENT APPLICATION NUMBER: US/10/148,328B

CURRENT FILING DATE: 1099-11-29

PRIOR PILING DATE: 1099-11-29

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-16-07

NUMBER OF SEQ ID NOS: 126

SOFTWARE: PALENTIN Ver. 3.2

SEQ ID NO 81

LENGTH: 1210
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Best Local Similarity 100.0%; Score 20, DB 8; Length 1210;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Origin of the sequence: soil organism US-10-148-328B-100
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ORGANISM: Unknown organism
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ORGANISM: Unknown organism
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US-10-148-328B-71

US-10-148-328B-71

Sequence 71, Application US/10148328B

GENERAL INFORMATION:
APPLICANT: JEANNIN, PRASCALE
APPLICANT: GUERINEAU, MICHEL
APPLICANT: SIMONET, PRASCALE
APPLICANTON: MCHELC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: MAPPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMFOUNDS
FILE REPERENCE: 03806.0547-0000NDS
FILE REPERENCE: 03806.0547-0000NDS
FILE REPERENCE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 2000-06-07
PRIOR PLICATION NUMBER: 60/209,800
PRIOR PLICATION NUMBER: 60/209,800
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin Ver: 3.2
SEQ ID NO 71
LENGTH: 1225
                                                                                                                                                                                                                             APPLICANT: PERMIN. PASCALE
APPLICANT: PERMODET, JERN-LUC
APPLICANT: PERMODET, JERN-LUC
APPLICANT: PERMODET, JERN-LUC
APPLICANT: SIMONET, PASCAL
APPLICANT: SIMONET, PASCAL
APPLICANT: SIMONET, PASCAL
TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
FILE REFERENCE: 03806.0547-00000
FILE REFERENCE: 03806.0547-00000
FILE REFERENCE: 2002-05-29
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: FR9915032
PRIOR APPLICATION NUMBER: ECT/FR00/03311
PRIOR APPLICATION NUMBER: 60/209, 800
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PATENTING NOWER: 50/209, 800
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SSQ ID NO 66
IENGTH: 1223
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ORGANIZAM: Unknown organism
FEATURE:
OTHER INFORMATION: Origin of the sequence: soil organism
                                                                                                                  RESULT 11
US-10-148-328B-66
Sequence 66, Application US/10148328B
GENERAL INFORMATION:
616 GCAAACAGGATTAGATACCC 635
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PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 76
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US-10-148-328B-67
                                                                                                                LENGTH:
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APPLICANT: JEANNIN, PASCALE
APPLICANT: PERNODET, JEAN-LUC
APPLICANT: BENNODET, JEAN-LUC
APPLICANT: SIMONET, PASCAL
TITLE OF INVENTION: METHED, PRESULTING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
FILE REFERENCE: 03806.047-00000
CURRENT APPLICATION NUMBER: US/10/148,328B
CURRENT FILING DATE: 2002-05-29
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APPLICANT: DEMNNIN, PASCALE
APPLICANT: PERMODET, JEAN-LUC
APPLICANT: GURRINEAU MICHEL
APPLICANT: SIMONET, PASCAL
TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: SEMULE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
CURRERRACE: 03806.0547-00000
CURRERRY APPLICATION NUMBER: 02,10/148,328B
CURRENT FILING DATE: 2002-05-29
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                                                     Query Match
100.0%; Score 20; DB 8; Length 1225;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels (
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/FR00/03311
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/209,800
PRIOR FILING DATE: 2000-66-07
NUMBER OF SEC ID NOS: 126
SOFTWARE: Patentin Ver. 3.2
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PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/209,800
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NAME/KEY: modified_base

LOCATION: (435)

OTHER INFORMATION: variable nucleotide
US-10-148-328B-98
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 98, Application US/10148328B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCAAACAGGATTAGATACCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Unknown organism
                                                                                                                                                                                                                                                                                                              RESULT 13
US-10-148-328B-98
        US-10-148-328B-71
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APPLICANT: PERNODET, JEAN-LUC
APPLICANT: STERNODET, JEAN-LUC
APPLICANT: GIBELINEAD, MICHEL
APPLICANT: GIBELINEAD, MICHEL
APPLICANT: GIBELINEAD, MICHEL
TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: SAMPLE, REGULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
FILE REFERENCE: 03806.0547-0000
CURRENT APPLICATION NUMBER: US/10/148,328B
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: FR9915032
PRIOR APPLICATION NUMBER: FR9915032
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE PATENTIN VOR: 3.2
SEQ ID NO 67
LENGTH: 1237
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100.0%; Score 20; DB 8; Length 1236;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 20; DB 8; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism US-10-148-328B-67
                                                        FEATURE:
, OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: August 4, 2004, 11:43:43 Job time : 200.036 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 67, Application US/10148328B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               653 GCAAACAGGATTAGATACCC 672
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ORGANISM: Unknown organism
TYPE: DNA
ORGANISM: Unknown organism
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US-10-425-115-28998/c

Sequence 28996, Application US/10425115

GENERAL INFORMATION: Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (53222) B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 28998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-10-425-115-29000

| Sequence 29000, Application US/10425115
| SEQUENCE 29000, Application US/10425115
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Cao, Yongwei
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants
| FILE REFERENCE: 38-21(53222) B
| CURRENT APPLICATION NUMBER: US/10/425,115
 Sequence 70573, A Sequence 4317, A Sequence 4316, Ap Sequence 125836, A Sequence 160109, Sequence 160109, Sequence 26387, A Sequence 21759, A Sequence 21759, A Sequence 103379, Sequence 153306, A Sequence 153306, A Sequence 153306, A Sequence 153306, A Sequence 992221, A Sequence 992221, A Sequence 13537, A Sequence 13537, A Sequence 13537, A Sequence 153306,
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US-10-425-115-70573
US-10-767-701-22517
US-09-39-72064-4333
US-10-425-115-125836
US-10-425-115-198986
US-10-425-115-198986
US-10-425-115-198986
US-10-425-115-12769
US-10-620-246-5
US-10-70-248-40085
US-10-425-115-13336
US-10-425-115-13336
US-10-767-701-13537
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100.0%; Pred. No. 0.71;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(850)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
    TYPE: DNA ORGANISM: Zea mays FEATURE: NAME/KEY: UNSULE
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Best Local Similarity
  775.0
    LENGTH:
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Matches
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247.629 Million cell updates/sec
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                                                                                         August 4, 2004, 06:43:54; Search time 199.036 Seconds
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1. /cgn2_6/ptodate/2/pna/USO6_NEW_COMB.seq:*

2. /cgn2_6/ptodate/2/pna/USO6_NEW_COMB.seq:*

3. /cgn2_6/ptodate/2/pna/USO7_NEW_COMB.seq:*

5. /cgn2_6/ptodate/2/pna/USO9_NEW_COMB.seq:*

5. /cgn2_6/ptodate/2/pna/USO9_NEW_COMB.seq:*

6. /cgn2_6/ptodate/2/pna/USO0_NEW_COMB.seq:*

7. /cgn2_6/ptodate/2/pna/USIO_NEW_COMB.seq:*

8. /cgn2_6/ptodate/2/pna/USIO_NEW_COMB.seq:*

9. /cgn2_6/ptodate/2/pna/USO0_NEW_COMB.seq:*

9. /cgn2_6/ptodate/2/pna/USO0_NEW_COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-425-115-109468
US-10-767-701-14989
US-10-767-701-15-150914
US-10-425-115-151509
US-10-767-701-22770
US-10-767-701-22770
US-10-767-701-28210
US-10-425-115-122047
US-10-425-115-122047
US-10-425-115-126075
US-10-674-124A-38
US-60-582-609-23584
US-60-582-609-23584
US-10-767-701-30539
US-10-430-201-4832
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                                                                OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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1 ggaggaaggcgagg
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1601
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Match 1
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Perfect score:
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No.
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Best Local Similarity 100. Matches 17; Conservative
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                                           TYPE: DNA; ORGANISM: Mus musculus
US-10-473-974-43
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Best Local Similarity
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ORGANISM: Zea mays
SEQ ID NO 43
LENGTH: 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Sequence 109468, Application US/10425115
Sequence 109468, Application US/10425115
Sequence 109468, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 109468
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GENERAL INFORMATION:
APPLICANT: GARCIA, TERESA
APPLICANT: ROWAN ROMAN, SERGIO
APPLICANT: TRAILEANER, JOACHEM
APPLICANT: THEILHABER, JOACHEM
APPLICANT: THEILHABER, JOACHEM
APPLICANT: THEILHABER, JOACHEM
APPLICANT: THEILHABER, SETENCH
APPLICANT: THEILHABER, SETENCH
APPLICANT: BUSHNELL, STEVEN
APPLICANT: BUSHNELL, STEVEN
APPLICANT: RAWADI, GEORGES
TITLE OF INVENTION: GEORGES
TITLE OF INVENTION: GEORGES
TITLE OF LINGUISTICALION NUMBER: US/10/473,974
CURRENT PILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: US/10/473,974
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                                                                                                                                                         CTHER INFORMATION: Clone ID: MRT4577_126459C.1
US-10-425-115-29000
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US-10-425-115-109468
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PRICA APPLICATION NUMBER: PCT/IB02/02211
PRICE PLING DATE: 2002-04-05
PRICE APPLICATION NUMBER: 60/281,400
PRICE FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 246
SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                      1853 GGAGGAAGGCGAGGATGA 1870
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     CURRENT FILING DATE: 2003-04
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 29000
LENGTH: 2551
                                                                                                    TYPE: DNA
ORGANISM: Zea mays
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ORGANISM: Zea mays
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US-10425-115-151508
US-10425-115-151508
Sequence 151508, Application US/10425115
Sequence 151508, Application US/10425115
Sequence 151508, Application US/10425115
GENERAL INFORMATION:
APPLICANT: Law. Young
APPLICANT: Zhou, Yihua
APPLICANT: Cav. Yongwei
APPLICANTON: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRESENCE: 38-21(5222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 151508
LENGTH: 2097
                                                                                                                                                                                                                                                                                                          Sequence 14989, Application US/10767701

Sequence 14989, Application US/10767701

Sequence 14989, Application US/10767701

September 14989, Application US/10767701

APPLICANT: Covariate, David K.

APPLICANT: Cao, Yondan

APPLICANT: Cao, Yondan

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: 1833518

CURRENT APPLICATION NUMBER: US/10/767,701

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 14989

LENGTH: 1847
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Query Match 85.0%; Score 17; DB 7; Length 1073; Best Local Similarity 100.0%; Pred. No. 2.6; Matches 17; Conservative 0; Mismatches 0; Indels
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US-10-767-701-14989
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US-10-425-115-151508
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LOCATION: (1)..(2097)
OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                        1005 GCAGGAAGCCGAGGATG 1021
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                                                                                                                                 1 GGAGGAAGGCGAGGATG 17
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Matches

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Enc., Yihaa
APPLICANT: Zhou, Yihaa
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5)222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/3-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 38956
LBNGTH: 551
TYPE: N.**
                     APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Diants and Uses Thereof For Plant Improvement
FITLE OF INVENTION: Diants and Uses Thereof For Plant Improvement
FILE REPERENCE: 38-21 (5335) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 28210
LENGTH: 510
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Rovalic, David K.
APPLICANT: CAO, Yilua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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100.0%; Pred. No. 9;
tive 0; Mismatches
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NAMB/KEY: unsure
LOCATION: (1)..(551)
CTHER INFORMATION: unsure at all n locations
FEATURE:
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                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: 7535963
US-10-767-701-28210
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Sorghum bicolor
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ses 16; Conserv
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ORGANISM: Zea mays
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT FILING DATE: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 130914
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Sequence 22770, Application US/10767701

Sequence 22770, Application US/10767701

GENERAL INFORMATION:

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

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8.9;
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    Indels
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US-10-425-115-130914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 80.0%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 8.5 Matches 16; Conservative 0; Mismatches
  Mismatches
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US-10-767-701-22770
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                     1592 GAGGAAGGCGAGGATGA 1608
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                                           2 GAGGAAGGCGAGGATGA
17; Conservative
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ORGANISM: Sorghum bicolor
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Best Local Similarity
Matches 16; Conserv
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Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
   16; Conservative
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       Matches
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Sequence 158496, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 158496
LENGTH: 1601
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19-10-425-115-126075/c

18-10-425-115-126075, Application US/10425115

18-10-425-115-126075, Application US/10425115

18-10-10-4204T: La Rosa, Thomas J.

19-10-4204T: La Rosa, Thomas J.

20-10-4204T: La Rosa, Thomas J.

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80.0%; Score 16; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 16; Conservative 0; Mismatches 0
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9.1;
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US-10-425-115-158496
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; OTHER INFORMATION: Clone ID: MRT4577_42791C.1
US-10-425-115-122047
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US-10-425_115-126075
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               NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 122047
LENGTH: 677
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Best Local Similarity
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ORGANISM: Zea mays
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                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
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Matches
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Gaps
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Sequence 38, Application US/10674124A

GENERAL INFORMATION:
APPLICANT: INFORMATION:
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
FILE REFERENCE: ORIN-033C19
CURRENT APPLICATION NUMBER: US/10/674,124A

CURRENT APPLICATION NUMBER: 10/257,511
PRIOR PILING DATE: 2003-09-7
PRIOR FILING DATE: 2003-09-7
PRIOR PILING DATE: 2000-04-13
PRIOR PILING DATE: 2000-04-13
PRIOR FILING DATE: 2002-09-28
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Sequence 297, Application US/10221714B
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DIEDENBROCK, Christian
APPLICANT: DIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Lumor suppressor genes and oncogenes
TITLE OF INVENTION: Lumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10013058.0
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10013058.0
PRIOR PILING DATE: 2000-04-07
PILING DATE: 2000-04-07
PILING DATE: 2000-04-07
PILING DATE: 2000-
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      Indels
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us-09-940-860-2.oligo.rnpn

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TYPE: DNA
CRANISM: Homo sapiens
CRANISM: Homo sapiens
CRANISM:
CREATURE:
CTHER INFORMATION: DISO7_10007639
FEATURE:
COTHER INFORMATION: Located on chromosome 1
COTHER INFORMATION: Located on chromosome 1
COTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
COTHER INFORMATION: sequence : 5692908
FEATURE:
COTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
COTHER INFORMATION: Sequence listing upward to telomere on chrosomal short arm and
COTHER INFORMATION: 5'-terminus of this base sequence : 168636
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Gaps ; 0 Ouery Match
75.0%; Score 15; DB 7; Length 144;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels

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Sequence 23, Appl.
Sequence 751, Appl.
Sequence 758, Appl.
Sequence 476, Appl.
Sequence 5, Appl.
Sequence 5, Appl.
Sequence 1, Appl.
Sequence 1, Appl.
Sequence 2, Appl.
Sequence 1, Appl.
Sequence 1, Appl.
Sequence 1, Appl.
Sequence 2, Appl.
Sequence 1, Appl.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 3, Appl.
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15, Appl
16, Appl
17, Appl
20, Appl
21, Appl
23, Appl
23, Appl
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Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09940860
| Publication No. US20040005555A1
| GENERAL INFORMATION:
| APPLICANT: Rothman, Richard
| APPLICANT: Majmadar, Maulik
| TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
| TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
| TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
| CURRENT APPLICATION NUMBER: US/09/940, 860
| CURRENT FILING DATE: 2001-08-29
| PRIOR APPLICATION NUMBER: 60/229,376
| PRIOR APPLICATION NUMBER: 60/229,376
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: FREUSEQ FOR WINDOWS Version 4.0
US-10-343-319-89

US-10-343-319-89

US-10-343-319-90

US-10-343-319-98

US-10-343-319-98

US-10-343-319-102

US-10-343-319-102

US-10-343-319-104

US-10-343-319-105

US-10-343-319-105

US-10-410-040A-19

US-10-410-040A-17

US-10-410-040A-21

US-10-879-536-755

US-10-879-536-755

US-10-213-878-5

US-10-213-878-5

US-10-213-878-5

US-10-213-878-5

US-10-213-878-5

US-10-213-878-5

US-10-377-297-5

US-10-377-297-5

US-10-837A-7

US-10-10-213-878-7

US-10-168-337A-7
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// Publication No. US20040077015A1
// GENERAL INFORMATION:
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                                                                                                                                                                                                                                            SEQ ID NO 1
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                                                                                                       August 4, 2004, 07:44:29; Search time 180.964 Seconds (without alignments) 541.892 Million cell updates/sec
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Sequence 76,
Sequence 77,
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Sequence 80,
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Sequence 1,
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| Can2 6/ptodata/2/pubpna/US07 PUBCOMB seq:*
| Can2 6/ptodata/2/pubpna/US07 PUBCOMB seq:*
| Can2 6/ptodata/2/pubpna/US06 PUBF PUB seq:*
| Can2 6/ptodata/2/pubpna/US06 PUBF PUB seq:*
| Can2 6/ptodata/2/pubpna/US07 NTW PUB seq:*
| Can2 6/ptodata/2/pubpna/US08 PUBCOMB seq:*
| Can2 6/ptodata/2/pubpna/US08 PUBCOMB seq:*
| Can2 6/ptodata/2/pubpna/US08 PUBCOMB seq:*
| Can2 6/ptodata/2/pubpna/US09A PUBCOMB seq:*
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| Can2 6/ptodata/2/pubpna/US09B PUBCOMB seq:*
| Can2 6/ptodata/2/pubpna/US09A PUBCOMB seq:*
| Can2 6/ptodata/2/pubpna/US09A PUBCOMB seq:*
| Can2 6/ptodata/2/pubpna/US09 NEW PUB seq:*
| Can2 6/ptodata/2/pubpna/US10A PUBCOMB seq:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-715-220-1
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US-10-343-319-81
US-10-343-319-83
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                                                                            - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length
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nes 20; Conserv
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APPLICANT: Vojdani, A.

TITLE OF INVENTION: DETECTION OF WYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: CHRONIC FAIIGUE SYNDROME AND RELATED DISORDERS
FILE REPERENCE: IMSCT.009A
CURRENT APPLICATION NUMBER: US/10/715,220
CURRENT APPLICATION NUMBER: US/9/283,655
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASLSEQ for Windows Version 3.0
LENGTH: 25
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US-10-343-319-76

Sequence 76, Application US/10343319

Publication No. US20040072242A1

GENERAL INFORMATION:

APPLICANT: Hunter, Neil

APPLICANT: Martin, Fjelda E.

APPLICANT: Martin, Fjelda E.

TITLE OF INVENTION: A METHOD OF DETECTING MICRORGANISMS

FILE REFERENCE: DAVISON OWARE: US/10/343,319

CURRENT FILING DATE: 2003-09-17

PRIOR APPLICANION NUMBER: PCT/AU01/00933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09940860; Publication No. US2004000555A1
GENERAL INFORMATION:
GAPLICANT: Nothman, Richard; APPLICANT: Rothman, Richard; APPLICANT: Rothman, Molecular DIAGNOSIS OF BACTEREMIA; FITUE REPERENTS: 0107,00185; CURRENT APPLICATION WOMBER: US/09/940,860; CURRENT FILING DATE: 2001-08-29; PRIOR APPLICATION NUMBER: 60/229,376; PRIOR APPLICATION NUMBER: 60/229,376; PRIOR APPLICATION NUMBER: 60/229,376; PRIOR FILING DATE: 2000-08-31; NUMBER OF SEQ ID NOS: 7; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 6; IENGTH: 30
                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Synthetic oligonucleotide primer US-10-715-220-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: synthetic amplification primer US-09-940-860-6
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Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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Publication No. US20040072242A1
Publication No. US20040072242A1
GENERAL INPORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Martin, Fjelda E.
FILE REFERENCE: DAVI139.002APC
CURRENT FILING DATE: 2000.9-17
PRIOR PILING DATE: 2000.9-17
PRIOR PILING DATE: 2000.07-28
NUMBER OF SEQ ID NOS: 106
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
LENGTH: 50
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APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVIL39.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR FILING DATE: 2001-07-27
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! LOCATION: (0) ...(0)
CTHER INFORMATION: Helicobacter pylori also.
US-10-343-319-76
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: AU PQ9090/2000
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTHARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 50
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Publication No. US20040072242A1
GENERAL INFORMATION:
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ORGANISM: Campylobacter jejuņi
FEATURE:
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US-10-343-319-77
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                                                                                                                             Length 50;
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APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Mardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS.
FILE REPERENCE: DAVIL139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT APPLICATION NUMBER: PCT/AU01/00933
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR PLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82
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APPLICANT: Hunter, Neil
APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Mardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS:
FILE REPERENCE: DAVI139.00APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
FRICR APPLICATION NUMBER: PCT/AU01/00933
FRICR APPLICATION NUMBER: AD P09090/2000
FRICR APPLICATION NUMBER: AU P09090/2000
FRICR APPLICATION NUMBER: AU P09090/2000
FRICR SEQ ID NOS: 106
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                        Score 20; DB 12;
Pred. No. 0.024;
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                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-10-343-319-82
; Sequence 82, Application US/10343319
; Bublication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
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     ; LENGTH: 50
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-319-81
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; ORGANISM: Haemophilus influenzae
US-10-343-319-83
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Best Local Similarity 100.0
Local 20; Conservative
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LENGTH: 50
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i Sequence 80, Application US/10343319

i Publication No. US20040072242A1

i CENERAL INFORMATION:

APPLICANT: Hunter, Neil

APPLICANT: Martin, Fjelda E.

APPLICANT: Markani, Amangla A.

TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS

FILE REFERENCE: DAVI139.002APC

CURRENT APPLICATION NUMBER: PCI/AU01/00933

PRIOR PILING DATE: 2000-07-27

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 106

SOFTWARE: PSSESSE for Mindows Version 4.0

LENGTH: SO

TUDD NO 80

LENGTH: SO

TUDD NO 80

THOSE NOS: 106
                                                                                                                                                                                                                                               Query Match
100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.024;
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APPLICANT: Hunter, Neil
APPLICANT: Hartin, Fjeldas A.
APPLICANT: Martin, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS;
FILE REFERENCE: DAVIJ39.003APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR PELICATION NUMBER: CT/AU01/00933
PRIOR PELICATION NUMBER: 2000-07-27
PRIOR PELICATION NUMBER: 2000-07-27
PRIOR PELICATION NUMBER: 2000-07-28
SPIOR PELICATION NUMBER: AU PQ9090/2000
PRIOR PELICATION NUMBER: 2000-07-28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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PRIOR APPLICATION NUMBER: AU PQ9090/2000
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SSCTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 79
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Thiomicrospira denitrificans US-10-343-319-80
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Publication No. US20040072242A1
GENERAL INFORMATION:
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                                                                                                                                             TYPE: DNA
, ORGANISM: Leptothrix mobilis
US-10-343-319-79
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Best Local Similarity 100.0
Matches 20; Conservative
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APPLICANT: Jacques, Nicholas B.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
TILE REFERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
FRICR PILING DATE: 2003-09-17
PRICR PLING DATE: 2001-07-27
PRICR APPLICATION NUMBER: PCT/AU01/00933
PRICR APPLICATION NUMBER: BCT/AU01/00933
PRICR APPLICATION NUMBER: AU PQ9090/2000
PRICR PLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
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APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Mardani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REPERENCE: DAVILLE O. DOZAPC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT APPLICATION NUMBER: PCT/AUO1/00933
PRIOR PLLING DATE: 2001-07-27
PRIOR PLLING DATE: 2000-07-28
NHOR FILING DATE: 2000-07-28
NHOR FILING DATE: 2000-07-28
NHOR FILING DATE: 2000-07-28
NHOR FILING DATE: 2000-07-28
SOFTWARE: FastSEQ for Windows Version 4.0
100.0%; Score 20; DB 12; Length ilarity 100.0%; Pred. No. 0.024; Conservative 0; Mismatchin
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                                                                                                                                                                                                                                                                         US-10-343-319-87
; Sequence 87, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
                                                                                                                                                             16 GCAAACAGGATTAGATACCC 35
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; ORGANISM: Caulobacter vibrioides
US-10-343-319-88
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Matches 20;
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APPLICANI: JACQUES, NICHOLAS A.
APPLICANT: JACQUES, NICHOLAS A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Nardkani, Mangala A.
ITILE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139,002APC
CURRENT PELLION: A METHOD OF DETECTING MICROORGANISMS
FILE REPERENCE: DAVI139,002APC
CURRENT FILING DATE: 2003-09-17
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FASESEQ FOR WINDOWS Version 4.0
SEQ ID NO 85
LENGTH: 50
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Sequence 84, Application US/10343319;
Publication No. US2040072242A1;
GENERAL INPORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Marchin, Fielda E.
APPLICANT: Marckani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002407.
FILE REFERENCE: DAVI139.002407.
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28

SOFTWARE: FSEC ID NOS: 106
SOFTWARE: FSEC ID NOS: 106
SEC ID NO 84

SEC ID NO 84

SEC ID NO 84
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Pred. No.
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Publication No. US20040072242A1
GENERAL INFORMATION:
APPLICANT: HUNCEY, Neil
                                                                                                                                   1 GCAAACAGGATTAGATACCC 20
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Best Local Similarity 100.0%;
Matches 20; Conservative 0.
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; ORGANISM: Escherichia coli
US-10-343-319-84
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ORGANISM: Salmonella typhi
                                                                                     20; Conservative
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Matches 20; Conserv
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US-10-343-319-85
                                      Query Match
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100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels
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US-10-343-319-89
i Sequence 89, Application US/10343319
j Sequence 80, Application US/10343319
j Publication No. US20040072242A1
j GENERAL INFORMATION:
    APPLICANT: Hunter, Nail
    APPLICANT: Martin, Fjelda E.
    APPLICANT: Martin, E.
    APPLICANT: Martin, Fjelda E.
    APPLICANT: Martin, Fjelda E.
    APPLICANT: Martin, E.
    APPLICANT: Martin, E.
    APPLICANT: Martin, E.
    APPLICANT: Martin, E.
    APPLICANTON NUMBER: PCT/AU01/00933
    PRIOR FILING DATE: 2000-07-28
    PRIOR FILING DATE: 2000-07-28
    NUMBER: PS SEQ ID NOS: 106
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 89
    LEMATH: SO
    TYPE: DNA
    ORGANISM: Nitrobacter winogradskyi
    US-10-343-319-89
16 GCAAACAGGATTAGATACCC 35
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Search completed: August 4, 2004, 11:56:21 Job time: 180.964 secs

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RESULT 2
US-09-940-860-7
Sequence 7, Application US/09940860
Publication No. US20040005555A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 20; Conservative
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Sequence 11, Appli
Sequence 11, Appl
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Sequence 5, Appli
Sequence 6, Appli
Sequence 4575, Appli
Sequence 25445, Appli
Sequence 32781, Appli
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                                                                                                                                                                                     August 4, 2004, 07:44:29; Search time 180.964 Seconds (without alignments) 541.892 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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11 US-09-940-866-2

13 9 US-09-728-74-11

14 US-10-719-633-11

15 10 US-10-719-633-11

16 US-10-289-762-1

17 US-10-289-762-1

17 US-10-437-96-25445

17 US-10-437-96-25445

17 US-10-437-96-25445

18 US-10-425-114-32946

19 US-10-425-114-32781

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11 US-10-389-493-35514

12 US-10-389-38-35514
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Maximum DB
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Sequence 297, App Sequence 28084, A Sequence 5759, Ap Sequence 5759, Ap Sequence 5759, Ap Sequence 504, App Sequence 504, App Sequence 506, App Sequence 508, App Sequence 503, App Sequence 513, App Sequence 513, App Sequence 513, App Sequence 14381, App Sequence 2152, App Se
                                           Sequence 15935,
Sequence 72402,
3 US-10-425-114-15476
3 US-10-425-114-1318
3 US-10-425-114-3138
3 US-10-437-963-72402
3 US-10-437-963-72402
3 US-10-437-963-72402
4 US-10-431-963-26084
4 US-09-923-876-5759
4 US-09-923-876-5759
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4 US-09-922-293-989
5 US-09-922-293-989
5 US-09-922-293-989
5 US-09-922-293-989
5 US-09-922-293-504
5 US-09-922-293-508
5 US-09-914-353-14381
5 US-09-814-353-14381
5 US-09-914-353-1937
7 US-09-914-353-1937
7 US-09-914-353-1937
7 US-09-914-353-7937
7 US-09-914-353-7937
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7 US-09-918-842A-2337
7 US-09-938-842A-2377
7 US-10-77-632-2366+33
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Gaps
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VG-09-940-860-2

Sequence 2, Application US/09940860

Publication No. US2004005555A1

GENERAL INFORMATION:

APPLICANT: Rothman, Richard

APPLICANT: Majmudar, Maulik

TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA

FILE REFERENCE: 01107.00185

CURRENT FILING DATE: 2001-08-29

PRIOR FILING DATE: 2000-08-29

PRIOR FILING DATE: 2000-08-31

NUMBER OF SEQ ID NOS: 7

SOFTWARRE: FASLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 11; 100.0%; Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: synthetic amplification primer US-09-940-860-2
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LENGTH: 1230025
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100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09726774

Patent No. US20020082256A1

Patent No. US20020082256A1

FROBRAL INFORMATION:

APPLICANT: INFORMATION:

TITLE OF INVENTION: Composition

FILE REFERENCE: 0450-0032.30

CURRENT FILING DATE: 2000-11-29

PRIOR APPLICATION NUMBER: US 60/168,150

PROBLEM FILING DATE: 1999-11-29

NUMBER OF SEQ ID NOS: 139

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 1548
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Publication No. US20040137485A1
GENERAL INFORMATION:
TTILE OF INVENTION: Patrick L.
TTILE OF INVENTION: Composition
FILE REFERENCE: 0450-0032.30
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US/10/719,633
CURRENT APPLICATION NUMBER: US/09/726,774
PRIOR APPLICATION NUMBER: US 60/168,150
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 139
APPLICANT: Rothman, Richard
APPLICANT: Majmudar, Maulik
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FILE REPERENCE: 01107.00185
CURRENT FILING DATE: 2001-08-29
FRICH REPLICATION NUMBER: 60/229,376
PRIOR APPLICATION NUMBER: 60/229,376
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 30
                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: synthetic amplification primer US-09-940-860-7
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ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-719-633-11
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Sequence 1, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Majmudar, Maulik
TITLE OP INVENTION: MOJECULAR DIAGNOSIS OF BACTEREMIA
FILE REFERENCE: 01107,00185
CURRENT APPLICATION NUMBER: US/09/940,860
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/229,376
PRIOR FILING DATE: 2000-08-31
NUMBER: OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11 LENGTH: 1548
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US-09-940-860-5
Sequence 5, Application US/09940860
Publication No. US20040005555A1
GENERAL INFORMATION:
APPLICANT: Rothman, Richard
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LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g
                                                                                    ; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-10-719-633-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Chlamydia trichomatis
US-09-940-860-5
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ORGANISM: Chlamydia pneumoniae
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NAME/KEY: misc_feature
LOCATION: (1)...(15000)
OTHER INFORMATION: n=a or c
FEATURE:
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OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (270001)..(285000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (285001)..(300000) OTHER INFORMATION: n=a or c or g or t LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or FEATURE: or or or ы Б or ö ö FEATURE:
NAME/KEY: misc_feature
LOCATION: (60001) .. (75000)
OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (75001)..(90000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (90001)..(105000) JTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (105001)..(120000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (120001)..(135000) OTHER INFORMATION: n=a or c or g WANE/KEY: misc feature GCCATION: (150001)..(165000) THER INFORMATION: n=a or c or g AAME/KEY: misc feature LOCATION: (165001)..(180000) THER INFORMATION: n=a or c or g VAME/KEY: misc feature LOCATION: (210001)..(225000) THER INFORMATION: n=a or c or g FEATURE:
NAME/KEY: misc_feature
LOCATION: (255501)..(24000)
OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (240001)..(255000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (45001)...(60000) OTHER INFORMATION: n=a or c or g AAME/KEY: misc feature LOCATION: (180001)..(195000) THER INFORMATION: n=a or c or g FEATURE:
NAME/KEY: misc_feature
LOCATION: (25501)..(270000)
OTHER INFORMATION: n=a or c or or o H VAME/KEY: misc feature LOCATION: (135001)..(150000) OTHER INFORMATION: n=a or c VAME/KEY: misc feature LOCATION: (195001)..(210000) OTHER INFORMATION: n=a or c NAME/KEY: misc_feature LOCATION: (300001)..(315000)

FEATURE:

FEATURE:
NAME/KEY: misc_feature
LOCATION: (375501)..(390000)
OTHER INFORMATION: n=a or c or g or t MANE/KEY: misc feature LOCATION: (33001)..(345000) OTHER INFORMATION: n=a or c or g or t FEATURE:
NAME/KEY: misc_feature
LOCATION: (360001) .(375000)
OTHER INFORMATION: n=a or c or g or t or g or t NAME/KEY: misc feature LOCATION: (49501)..(510000) JTHER INFORMATION: n=a or c or g or NAWE/KEY: misc feature LOCATION: (510001)..(525000) OTHER INFORMATION: n=a or c or g or FEATURE:
NAME/KEY: misc_feature
LCCATION: (55501)..(57000)
OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (420001)..(435000) OTHER INFORMATION: n=a or c or g or FEATURE:
NAMES/KEY: misc_feáture
CCCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (390001)..(405000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (315501)..(330000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (435001)..(450000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc_feature LCCATION: (450001)...(465000) OTHER INFORMATION: n=a or c or g FRATURE. NAME/KEY: misc feature LOCATION: (480001)..(495000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (46501)..(480000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (405001)..(420000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (525001)..(540000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (54001)..(555000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (345001)..(360000) OTHER INFORMATION: n=a or c

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 4673
LENGTH: 1143
                                                                                                                                                                                                                                                                                                   APPLICANT: Li, Find
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 25445
LENGTH: 2738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.0%; Score 18; DB 17; Length 2738; 100.0%; Pred. No. 0.59; tive 0; Mismatches 0; Indels (
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US-10-437-963-25445
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US-10-437-963-4673
                       Sequence 25445, Application US/10437963
PUDLIcation No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Bouk Wei
APPLICANT: Bukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4673, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Oryza sativa
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Soren, Yihua
APPLICANT: Soren, Steven E
APPLICANT: Soren, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Soren, Sorgen E
APPLICANT: Sorgen E
APPLICANT: Nordence Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313) B
CURRENT FILING: DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 4575
LENGTH: 2123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 16; Length 1230025; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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90.0%; Score 18; DB 13; Length 2123;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 18; Conservative 0; Mismatches 0; Indels
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US-10-425-114-4575
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NAME/KEY: misc feature
LOCATION: (58501)..(600000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                           NAME/KEY: misc feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc feature
LOCATION: (67501)...(690000)
OTHER INFORMATION: n=a or c or g or FEATURE:
                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (64501)..(660000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4575, Application US/10425114; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or
                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGAGGAAGGCGAGGATGACG 20
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Matches 20; Conservative
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ORGANISM: Zea mays
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HINKLE, Gregory J.

APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
FRIOR APPLICATION NUMBER: US 60/360,039
FRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 35514
LENGTH: 2145
TYPE: NUMBER: NUMBE
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; Sequence 25403, Application US/204003488A1
; Sequence 25403, Application No. US2004003488A1
; Publication No. US2004003488A1
; APPLICANT: Liu, Jingdong
; APPLICANT: Liu, Jingdong
; APPLICANT: Cao, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (5313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25403
; LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 2.2;
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100.0%; Pred. No. 11;
cive 0; Mismatches 0; Indels
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100.0%; Pred. No. ...
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Carlos
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0°;
100.0°; ±1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GAAGGCGAGGATGACG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA; CRGANISM: Mesorhizobium loti
US-10-369-493-35514
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Best Local Similarity 100.(
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM: Zea mays
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yes-10-425-114-54(B1/C)
yes-10-425-114
yes-10 No. US2004003488BA1
yebblication No. US200400348BBA1
general INFORMATION:
general Information:
hebblicant: Lib, Jingdong
yes-10-10 No. Yilua
yes-10-10 No. Yilua
yes-10-10 No. Yilua
yes-10 No. Yilua
yes-10-10 No. Yilua
yes-10-10 No. Yilua
yes-10-10 No. Yilua
yes-10 No. Yorgwei
yes-10 N
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Sequence 32946, Application US/10425114
Sequence 32946, Application US/10425114
Sequence 32946, Application US/10425114
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: End, Yihua
APPLICANT: Screen, Staven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: GF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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85.0%; Score 17; DB 13; Length 1305;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CTHER INFORMATION: Clone ID: UC-ZMFLMO17043F07_FLI US-10-425-114-32946
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US-10-425-114-32781
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US-10-369-493-35514/c
; Sequence 35514, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1122 GAGGAAGGCGAGGATGA 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 GAGGAAGGCGAGGATGA 174
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Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-114-32781/c
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LENGTH: 1305
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Sequence 14476, Application US/10425114

Sequence 15476, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Stou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)8

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

EENGTH: 1543
APPLICANT: ITAMACK, COLLIA
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: You H.
TITLE OP INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERBNCE: ELITRA.034A
CURRENT FILING DATE: 2000-03-21
FRIOR PILING DATE: 2000-03-21
FRIOR PLICATION NUMBER: 60/191,078
FRIOR PLICATION NUMBER: 60/207,727
FRIOR PLING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR PLING DATE: 2000-05-26
FRIOR PLING DATE: 2000-09-06
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FRIOR PLING DATE: 2000-10-23
FRIOR PLING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-22
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80.0%; Score 16; DB 13; Length 1251;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels (
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CTHER INFORMATION: Clone ID: LIB3060-007-All_FLI

5/5-10-425-114-15476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Cornyebacterium diptheriae
US-10-282-122A-17957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403 GAGGAAGGCGAGGATG 418
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ORGANISM: Zea mays
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Gaps
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                          0; Indels
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100.08; Pre-
                                                                            330 daggaaggcgaggarg 315
           Best Local Similarity 100.
Matches 16; Conservative
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/pna/US102A_C /pna/US102B_C /pna/US103A_C /pna/US103B_C /pna/US104A_C /pna/US104B_C /pna/US104B_C /pna/US104B_C

Run on:

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(9912 - 6) prodated 2/ pina/U8102B_COMB.seq:
(9912 - 6) prodated 2/ pina/U8104B_COMB.seq:
(9912 - 6) prodated 2/ pina/U8101 COMB.seq:
(9912 - 6) prodated 2/ pina/U8104B_COMB.seq:
(9912 - 6) prodated 2/
                                                                                                                                                           August 4, 2004, 06:32:11; Search time 1825.78 Seconds (without alignments) 385.436 Million cell updates/sec
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(ggn2 6/ptodata/2/pna/NG06 COMB.seq:*
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(ggn2 6/ptodata/2/pna/NG09 COMB.seq:*
(ggn2 6/ptodata/2/pna/NG092 COMB.seq:*
(ggn2 6/ptodata/2/pna/NG092 COMB.seq:*
(ggn2 6/ptodata/2/pna/NG095 COMB.seq:*
(ggn2 6/ptodata/2/pna/NG098 COMB.seq:*
(ggn2 6
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/cgn2_6/ptodata/2/pna/US099F_COMB.seq:
/cgn2_6/ptodata/2/pna/US100A_COMB.seq:
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ptodata/2/pna/US099B_COMB.seq:
ptodata/2/pna/US099C_COMB.seq:
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37577330 segs, 17593059518 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                   - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
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Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Query Match 100.0%; Score 20; DB 39; Length 20; Best Local Similarity, 100.0%; Pred. No. 2; Matches 20; Conservative 0; Mismatches 0; Indels

1 GGAGGAAGGCGAGGATGACG 20

GGAGGAAGGCGAGGATGACG 20

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; OTHER INFORMATION: synthetic amplification primer US-09-940-860-2
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 5,
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GENERAL INFORMATION: Richard

APPLICANT: Rothman, Richard

APPLICANT: Madjundar, Maulik

TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA

FILE REPERBURG: 01107.00185

CURRENT APPLICATION NUMBER: US/09/940,860

CURRENT FILING DATE: 2001-08-29

PRIOR PELING DATE: 2000-08-31

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PASSEQ for Windows Version 4.0

LENGTH: 20
                                                                                                                                                      US-09-438-185-1
US-09-438-185A-1
US-10-219-999-18302
US-10-425-114-4575
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US-10-437-963-25445
US-09-702-134-21825
US-09-815-264-71774
US-09-620-392-33867
US-09-236-21887
US-09-236-21887
US-09-236-21887
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US-09-982-402-2609
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US-60-079-469-696
                                                                                                                           US-09-201-228A-1
US-10-289-762-1
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ORGANISM: Artificial Sequence
FEATURE:
                      Query
Match Length
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US-09-940-860-2
                                      Score
                      Result
No.
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 20; DB 39; Length 30; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 20; Conservative 0; Mismatches 0; Indels
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US-10-719-633-11
Sequence 11, Application US/10719633
Sequence 11, Application US/10719633
FILE NFORMATION:
TITLE OF INVENTION: Antisense Antibacterial Method and TITLE OF INVENTION: Composition
FILE REFERENCE: 0450-0032.30
CURRENT PAPLICATION NUMBER: US/10/719,633
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US/09/726,774
PRIOR APPLICATION NUMBER: US/09/726,774
PRIOR APPLICATION NUMBER: US/09/726,774
PRIOR APPLICATION NUMBER: US/09/726,774
PRIOR PILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 139
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH 1548
                               Sequence 7, Application US/09940860
; Sequence 7, Application US/09940860
; GENERAL INFORMATION:
; APPLICANT: Rothmar. Richard
; APPLICANT: Majundar. Maulik
; TITLE COF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REPRENCE: 01107.00185
; CURRENT APPLICATION NUMBER: 2001.08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; RICHARD APPLICATION NUMBER: 60/229,376
; NUMBER OF SEQ. ID NOS: 7
; SOFFWARE OF SEQ. ID NOS: 7
; SOFFWARE FREISEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-460-7
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; ORGANISM: Chlamydia trachomatis
US-10-719-633-11
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
RESULT 2
US-09-940-860-7
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7
LENGTH: 30
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Sequence 1. Application US/10289762

Sequence 1. Application US/10289762

GENERAL INFORMATION:

APPLICANT: Griffais, F.

TILLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment:
TILLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, previTILLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1

LENGTH: 1230025
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NAME/KEY: misc feature
LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (75001)..(90000)
THER INFORMATION: n=a or c or g or
FEATURE:
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LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g
FEATURE:
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NAME/KEY: misc feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (165001)..(180000)
OTHER INFORMATION: n=a or c or
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LLOCATION: (15001)..(30000)
OCHER INFORMATION: n=a or c or
PEATURE:
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or
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LCCATION: (135001)..(150000)
DTHER INFORMATION: n=a or c or
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Chlamydia pneumoniae
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LOCATION: (15001)..(165000)
OTHER INFORMATION: n=a or c
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LOCATION: (195001)..(210000)
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LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c
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LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or
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LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or
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NAME/KEY: misc_feature
                            US-10-289-762-1
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APPLICANT: Griffais, Remy
APPLICANT: Griffais, Remy
APPLICANT: Acquireky, Robert John
APPLICANT: Acquireky, Robert John
APPLICANT: Beck, Joel A.
APPLICANT: Peck, Joel A.
TITLE OF INVENTION: CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE
TITLE OF INVENTION: AND POLYPEPTIDES, FRACHENTS THEREOF AND USES THEREOF, IN
TITLE OF INVENTION: NPECTION
TITLE OF INVENTION: INFECTION
TITLE OF INVENTION: INFECTION
FILE REFERENCE: 9710-0004-99
CURRENT PILING DATE: 1998-11-30
PRIOR PILING DATE: 1998-11-04
PRIOR PILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: FR 97-15041
PRIOR PILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 5981
SOUTHARD: FRANCE PRICED FOR Windows Version 4.0
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100.0%; Score 20; DB 16; Length 1038608;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0;
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100.0%; Score 20, DB 39, Length 1550;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                 APPLICANT: Najmudar, Maulik
APPLICANT: Majmudar, Maulik
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FILE REFERENCE: 0.1107.0.0185
CURRENT APPLICATION NUMBER: 0.8/09/940,860
CURRENT FILING DATE: 2.001-08-29
PRIOR APPLICATION NUMBER: 60/229,376
PRIOR APPLICATION NUMBER: 60/229,376
PRIOR PILING DATE: 2.000-08-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1550
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GENERAL INFORMATION:
APPLICANT: Griffais, Remy
APPLICANT: Hoiseth, Susan K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)...(1038608)

OTHER INFORMATION: n = A,T,C or G
US-09-201-228A-1
                      Sequence 5, Application US/09940860 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Chlamydia trichomatis
US-09-940-860-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
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LENGTH: 1038608
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-09-940-860-5
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FEATURE:
NAME/KEY: misc feature
LOCATION: (210701)..(225000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (225001)..(240000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (465001)..(480000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (270001)..(285000)
DTHER INFORMATION: n=a or c or g or t
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LOCATION: (375\overline{0}000)
JTHER INFORMATION: n=a or c or g or t
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LOCATION: (420001)..(435000)
DTHER INFORMATION: n=a or c or g or t
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                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (255001)..(270000)
OTHER INFORMATION: n=a or c or g or
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OCATION: (300001)..(315000)
THER INFORMATION: n=a or c or g or
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LOCATION: (330001)..(345000)
JTHER INFORMATION: n=a or c or g or
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LOCATION: (390001)..(405000)
THER INFORMATION: n=a or c or g or
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NAME/KEY: misc feature
LOCATION: (435001)..(450000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (285001)..(300000)
JTHER INFORMATION: n=a or c or g
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LOCATION: (315001)..(330000)
THER INFORMATION: n=a or c or g
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LOCATION: (360001)..(375000)
JTHER INFORMATION: n=a or c or g
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LOCATION: (405001)..(420000)
JTHER INFORMATION: n=a or c or g
OTHER INFORMATION: n=a or c or g
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LOCATION: (345001)..(360000)
OTHER INFORMATION: n=a or c
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LOCATION: (45001)..(465000)
OTHER INFORMATION: n=a or c
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Gaps
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NAME/KEY: misc_feature
LOCATION: (67501)..(690000)
OTHER INFORWATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
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LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or
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NAMES KEY: misc feature
LOANIKEY: (51001). (525000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (525001)..(540000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (540001)..(555000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g or
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NAME/KEY: misc feature
LOCATION: (58501)..(600000)
OTHER INFORMATION: n=a or c or g or
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US-09-438-185-1
Sequence 1, Application US/09438185
; SENERAL INFORMATION:
; APPLICANT: Stephens, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGAGGAAGGCGAGGATGACG 20
FEATURE:
NAME/KEY: misc_feature
LOCATION: (480001)..(495000)
OTHER INFORMATION: n=a or c or g
FEATURE:
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LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g
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NAME/KEY: misc_feature
LOCATION: (64501)..(66000)
OTHER INFORMATION: n=a or c or
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MAMB/KEY: misc_feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c
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LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c
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NAME/KEY: misc feature
LOCATION: (55501).. (57000)
OTHER INFORMATION: n=a or c
                                                                                                                NAME/KEY: misc feature
LOCATION: (495001)..(510000)
OTHER INFORMATION: n=a or c
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Sequence 4575, Application US/10425114

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Ebou, Yihua
APPLICANT: Exeen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE REPERRENCE: 38-21 (5313)
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
LENGTH: L
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| Sequence 4575, Application US/10425114A
| GENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Zhou, Yihua
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Co. Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 020-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 18302
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red. No. 18;
Mismatches 0; Indels (
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18;
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US-10-425-114-4575
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Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
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Best Local Similarity 100.0
Warches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) NAME/KEY: CDS
; LOCATION: (161)..(1768)
; OTHER INFORMATION:
US-10-219-999-18302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
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ORGANISM: Zea mays
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                                                APPLICANT: Kalman, Sue
APPLICANT: Kalman, Sue
APPLICANT: All May Sue Superior Superi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Tavis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
CURRENT APPLICANION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
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PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: PastSEQ for Windows Version 3.0
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; ORGANISM: Chlamydia pneumoniae
US-09-438-185-1
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ORGANISM: Chlamydia pneumoniae
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APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-10-219-999-18302/c
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LENGTH: 1230230
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APPLICANT: Cochi, Jeffrey M.
APPLICANT: Koshi, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Mu, Wei
TILEO F INVENTION: Genomic Plant Sequences And Uses Thereof
FILE REFERENCE: 38-71 (5.1237) G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT APPLICATION NUMBER: US/09/815,264
FRIOR FILING DATE: 2000-07-19
FRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
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                                                                                               Query Match 90.0%; Score 18; DB 30; Length 13218; Best Local Similarity 100.0%; Pred. No. 17; Matches 18; Conservative 0; Mismatches 0; Indels 0
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; ORGANISM: Oryza sativa
; OTHER INFORMATION: unsure at all n locations
US-09-620-392-33867
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APPLICANT: Equkharov, Andrey A.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: McIninch, James
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/620,392
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 69652
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 71774, Application US/09815264
GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey A.
APPLICANT: Cao, Yongwei
APPLICANT: Dotson, Stanton B.
APPLICANT: Koshi, Jeffrey M.
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CRGANISM: Oryza sativa
US-09-815-264-71774
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-21825
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US-09-815-264-71774/c
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US-09-620-392-33867/c
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement,
FILE REFERENCE: 38-21(3321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 25445
LENGTH: 2738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Clone ID: PAT_MRT4530_30330C.1
US-10-437-963-25445
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Sequence 21825, Application US/09702134
GENERAL INFORMATION:
APPLICANT:
BOUKharov, Andrey A.
APPLICANT:
APPLICANT: Goo, Yongwei
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Hu, Jingdong
APPLICANT: MINinch, James
APPLICANT: Wu Wei
TITLE REPERENCE:
CURRENT APPLICATION NUMBER: US/09/702,134
CURRENT APPLICATION NUMBER: US/09/702,134
CURRENT APPLICATION NUMBER: US/09/702,134
CURRENT APPLICATION NUMBER: 2000-10-31
NUMBER OF SEQ ID NOS:
SEQ ID NO 21825

LABORTH: 13218
                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: 700382382_FLI
US-10-425-114A-4575
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING:DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 4575
LENGTH: 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25445, Application US/10437963
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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ORGANISM: Oryza sativa
                                                                                                                                                             TYPE: DNA ORGANISM: Zea mays
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Search completed: August 4, 2004, 11:29:54 Job time: 1831.78 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model	del.	
Run on: August 4, 2004, 04:03:11; Sea (wit	; Search time 963.229 (without alignments) 989.948 Million cell	Seconds updates/sec
Title: US-09-940-860-3 Perfect score: 22 Sequence: 1 acaaggcccgagaacgtattca 22	22	
Scoring table: OLIGO_NUC Gapop_60.0 , Gapext 60.0		
Searched: 3470272 seqs, 21671516995 resid	5 residues	
Word size : 0	2	
Total number of hits satisfying chosen paramete	parameters: 6940544	
Minimum DB seq length: 0 Maximum DB seq length: 200000000		
Post-processing: Listing first 45 summaries	ies	
GenEmbl:* 1; gb_ba:* 2; gb_htg:* 3; gb_ntg:* 4; gb_ov:* 6; gb_pt:* 10; gb_pt:* 10; gb_pt:* 11; gb_pt:* 12; gb_pt:* 13; gb_un:* 14; gb_vi:* 15; em_ba:* 15; em_ba:* 16; em_fun:* 17; em_hun:* 18; em_pt:* 22; em_ov:* 23; em_pt:* 24; em_pt:* 25; em_pt:* 25; em_pt:* 26; em_to:* 27; em_to:* 28; em_to:* 29; em_to:* 20; em_t		

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AF29495 Unculture	Uncult	Uncul	AY391670 Unculture	Sequen	AF257294 Unculture	AJZ41/80 Unidentii AF535201 Unculture	AF226208 Unculture	AY191889 Unculture	AF385928 Mobiluncu	AF289914 Unculture	AKU/1534 Sequence L09057 Unknown ana	AY038517 Unculture	ABU/Si68 Unculture AY261423 Unculture	AY090655 Unculture	AF423789 Uncurred	AJ241721 Unidentif	AF332350 Unculture AF429144 Unculture	Uncultur	AF429234 Unculture AY012521 Unculture	Unidenti	Uncul	AY217417 Unculture	Uncul	Uncul	Uncul	Uncul	ident	AY133110 Unculture	מסמון	Uncul	AY239537 Unculture			DNA linear BCT 10-JAN-2002 ribosomal RNA gene, partial				X. and May, H.D. that links its growth to the 5-chlorobiphenyl	
SUMMARIES	В ІО	AF294958					AF257294	m							1 ABU/5168 1 AY261423			m				AF027077		AY217417										ALIGNMENTS		236 bp OTU1 16S	19629	rium	ental samples.	Sowers, K. Joorganism (of 2,3,5,0)	=
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Uncultured green sulfur bacterium clone OTU 1 16S ribosomal RNA
AP389905
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Cutter,L.A., Watts,J.B.M., Sowers,K.R. and May,H.D.
Indications for acetate as the carbon source and electron donor in
anaerobic ortho PCB dechlorination
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Submitted (11-JUN-2001) Center of Marine Biotechnology, University of Maryland Biotechnology Institute, Columbus Center, 701 E. Pratt St., Baltimore, MD 21202, USA
Location/Qualifiers
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uncultured Chlorobi pacterium
Bacteria; Chlorobi;
1 (bases 1 to 260)
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/db.xref="taxon:156405"
/clone="GNU 1"
/note="DNA sequence from PCB-dechlorinating enrichment
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3 (bases 1 to 236)
Watts,J.E.M., Cutter,L.A., Sowers,K.R. and May,H.D.
Watts,J.E.M., Cutter,L.A., Sowers,K.R. and May,H.D.
Direct Submission
Submitted (11-AUG-2000) Center of Marine Biotechnology, 701
Pratt St., Baltimore, MD 21202, USA
Location/Qualifiers
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/db_xref="taxon:73429"
/note="OTU 1; PCB dechlorinating culture"
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Environ. Microbiol. 3 (11), 699-709 (2001)
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/product="168 ribosomal RNA"
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AY391637 302 bp DNA linear BCT 15-OCT-2003
Uncultured soil bacterium clone M21 16S ribosomal RNA gene, partial
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                                                                                                                                                                                                                                                                                                                                                                      Dacteria; environmental samples.

1 (bases 1 to 302)

2 (bases 1 to 302)

Microbiology community structure and diversity in a century-long manure-treated agroecosystem

Microbiology community structure and diversity in a century-long manure-treated agroecosystem

2 (bases 1 to 302)

Sun, H., Deng, S. and Raun, W.R.

Direct Submission

Submitted (16-525-2003) Plant and Soil Sciences, Oklahoma State University, 368 Ag Hall, Stillwater, OK 74078, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uncultured soil bacterium uncultured soil bacterium bacterium Bacteria; environmental samples.

1 (bases 1 to 302) Sun, H., Deng, S. and Raun, W.R. Microbiology community structure and diversity in a century-long manure-treated agroecosystem
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Unpublished
2 (bases 1 to 302)
2 (bases 1 to 302)
Sun,H., Deng,S. and Raun,W.R.
Direct Submission
Submished (16-SEP-2003) Plant and Soil Sciences, Oklahoma State Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State University, 368 Ag Hall, Stillwater, OK 74078, USA
University, 368 Ag Hall, Stillwater, OK 74078, USA
Location/Qualifiers
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/mol type="genomic DNA"
/isolation_source="total microbial community of
century-long manure-treated soil"
/db xef="taxon:164851"
/clone="M21"
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207 ACAAGGCCCGAGAACGTATTCA 186
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AY391637.1 GI:37624038
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AY391643.1 GI:37624044
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372 bp DNA linear BCT 09-JUL-2001
Uncultured marine gamma proteobacterium DHB-31 16S ribosomal RNA
AF257294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [Dages 1 to 372] [Dagez-Gopez,A., Moreira,D. and Rodriguez-Valera,F. Lopez-Garcia,P., Lopez-Lopez,A., Moreira,D. and Rodriguez-Valera,F. Submitsed (18-APR-2000) Microbiology, University Miguel Hernandez, Facultad de Medicina, Campus de San Juan, San Juan, Alicante 03550,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="uncultured marine gamma proteobacterium DHB-31"
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uncultured marine gamma proteobacterium DHB-31
Bacteria, Proteobacteria, Gammaproteobacteria, environmental
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100.0%; Pred. No. 3.9;
tive 0; Mismatches 0;
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100.0%; Score 22; DB 6;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 22; Conservative 0; Mismatches 0;
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1 (bases 1 to 370)

Dodge,D.E. and White,T.J.

Method for diagnosis of lyme disease

Patent: US 5912117-A 35 15-JUN-1999;

Location/Qualifiers
Method for diagnosis of lyme disease
Patent: US 5912117-A 36 15-JUN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           370 bp I
Sequence 35 from patent US 5912117.
AR071568
AR071568.1 GI:7222456
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/mol_type="unassigned DNA"
                                                      1. .368
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                             273 ACAAGGCCCGAGAACGTATTCA 252
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                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 22; Conservative
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AR071568/c
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AF257294/c
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SM uncultured soil bacterium
Bacteria; environmental samples.
E 1 (bases 1 to 309)
Sun,H., Deng,S. and Raun,W.R.
Microbiology community structure and diversity in a century-long manure-treated agreeocosystem
L Unpublished 309)
Sun,H., Deng,S. and Raun,W.R.
Sun,H., Deng,S. and Raun,W.R.
Direct submission
L Sun,H., Sersp-2003) Plant and Soil Sciences, Oklahoma State
University, 368 Ag Hall. Stillwater, OK 74078, USA
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Uncultured soil bacterium clone M54 16S ribosomal RNA gene, partial
sequence.
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/isolation_source="total microbial community of century.long manure-treated soil"
| bx xref="taxon:164851" | clone="M27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/isolation_source="total microbial community of century-long manure-treated soil"
/db_xref="taxon:164851"
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/product="168 ribosomal RNA"
                                                                                            <li..>302
/product="168 ribosomal RNA"
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Sequence 36 from patent US 5912117.
AR071569.1 GI:7222457
                                                                          /environmental_sample
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Unclassified.
1 (bases 1 to 368)
Dodge, D.E. and White, T.J.
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AY391670/c
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AR071569/c
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Matches 2
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Uncultured euglenid clone CD1H11 16S ribosomal RNA gene, partial
sequence.
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                                                                                                                                                                                                                                                       UNA 12-DEC-1999
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Unidentified microorganism 16S rRNA gene, partial, clone Cow39.
AJ241780
                                                                                                                             Gaps
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Submitted (14-APR-1999) Pryde S.E., Microbial and Intestinal
biology, Rowett Research Institute, Greenburn Road, Bucksburn,
Aberdeen, AB21 9SB, UK
Location/Qualifiers
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unidentified microrganism
unidentified microrganism
unclassified; environmental samples.
1 (bases 1 to 380)
Pryde,S.E., Richardson,A.J., Stewart,C.S. and Flint,H.J.
Molecular analysis of the microbial diversity present in the
colonic wall, colonic lumen, and cecal lumen of a pig
Appl. Environ. Microbiol. 65 (12), 5372-5377 (1999)
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                                                                                               100.0%; Score 22; DB 1; Length 372; 100.0%; Pred. No. 3.9; tive 0; Mismatches 0; Indels
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uncultured euglenid
Eukaryota; Euglenozoa; environmental samples.
I (bases 1 to 420)
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                                        <1. .>372
/product="165 ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <1. .>380
/gene="16S rRNA"
/product="16S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
/mol_type="genomic DNA"
/db_xref="taxon:123962"
/clone="DHB-31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="taxon:81726"
/clone="Cow39"
                                                                                                                                                                      259 ACAAGGCCCGAGAACGTATTCA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 ACAAGGCCCGAGAACGTATTCA 267
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                                                                                                                                                                                                                                                                                                 AJ241780.1 GI:6066808
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Pryde, S.E.
                                                                                                                           Conservative
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Best Local S
Matches 22
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Bacteria; environmental samples.
1 (bases 1 to 431)
Chelius,M.K. and Triplett,E.W.
The Diversity of Archaea and Bacteria in Association with the Roots of Zea mays L
Microb. Ecol. 41 (3), 252-263 (2001)
Frias-Lopez,J., Zerkle,A.L., Bonheyo,G.T. and Fouke,B.W. Partitioning of bacterial communities between seawater and healthy, black band diseased, and dead coral surfaces Appl. Environ. Microbiol. 68 (5), 2214-2228 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF226208 431 bp DNA linear BCT 28-MAY-2002 Uncultured maize root bacterium Zmrc163 16S ribosomal RNA gene,
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                                                                                                                                  2 (bases 1 to 420)
Frias-Lopez, J., Zerkle, A.L., Bonheyo, G.T. and Fouke, B.W.
Direct Submission
Submitted (06-AUG-2002) Department of Geology, University of
Illinois at Urbana-Champaign, 1301 W. Green Street, Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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    431
    /organism="uncultured maize root bacterium Zmrc163"

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                                                                                                                                                                                                                                                                                                                                   1. .420
/organism="uncultured euglenid"
/mol_type="genomic DNA"
/isolation_source="marine"
/db_xref="texon:167168"
/clone="CD1H11"
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/product="168 ribosomal RNA"
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/product="16S ribosomal RNA"
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Chelius, M.K. and Triplett, E.W.
Direct Submission
Submitted (19-JAN-2000) Agronomy, Un
1575 Linden Dr., Madison, WI 53706,
Location/Qualifiers
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/db_xref="taxon:121653"
/clone="Zmrc163"
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AF226208
AF226208.1 GI:7716143
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uncultured green non-sulfur bacterium Kmlps6-20
uncultured green non-sulfur bacterium Kmlps6-20
Bacteria, Chloroflexi, environmental samples.
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Pred. No. 3.6;
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/product="168 ribosomal RNA"
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strain="ATCC35243"
/db_xref="ATCC:35243"
/db_xref="taxon:2052"
<1. .>473
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                                                    BCT 10-MAR-2003
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Bacterial distribution and phylogenetic diversity in the Changjiang estuary before the construction of the Three Gorges Dam
Microb. Ecol. 43 (1), 82-91 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sekiguchi, H. and Uchiyama, H.
Sekiguchi, H. and Uchiyama, H.
Direct Submission
Submitted (05-APR-2000) Hiroyuki Sekiguchi, National Institute for
Environmental Studies, Water Environmet Quality; Onogawal6-2,
Tsukuba, Ibaraki 305-0053, Japan (E-mail:seki@nies.go.jp,
Tel:81-298-50-2412, Fax:81-298-50-2576)
                                                                                                                                                                                                                                                                                                      Unpublished

2 (bases 1 to 432)

2 (bases 2 to 432)

2 (bases 2 to 432)

Diacut, R.E., Languer, H.W. and Inskeep, W.P.

Direct Submission

Submitted (06-DEC-2002) Land Resources and Environmental Sciences, Montana State University - Bozeman, Leon Johnson Hall, Bozeman, MT
                                                                                                                                                        uncultured bacterium
uncultured bacterium
bacteria; environmental samples.
1 (Dases I to 432)
Macur, R.E., Languer, H.W. and Inskeep, W.P.
Molecular analysis of microbial communities in
acid sulfate-chloride-arsenic geothermal springs in Yellowstone
National Park
                                                  AY191889 432 bp DNA linear BCT 10-MAR
Uncultured bacterium clone BG6 168 ribosomal RNA gene, partial
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/mol type="genomic DNA"
/isolation_source="acid-sulfate-chloride-arsenic
geothermal spring"
/db_xref="taxon:77133"
/clone="BG6"
/environmental sample
/country="USA: Wyoming, Yellowstone National Park"
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/product="168 ribosomal RNA"
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uncultured bacterium ECS7
Bacteria, environmental samples.
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AY191889.1 GI:28396218
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AB041277.1 GI:10716064
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497 bp DNA linear BCT 09-APR-2001
Uncultured green nonsulfur bacterium Kmlps6-20 16S ribosomal RNA
Gene, partial sequence.
AF289914
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2 (bases 1 to 473)

Park, H., Kim, C., Choi, H., Jang, H. and Kim, H.

Direct Submission
Submitted (25-MAY-2001) SJ Hightech Co., Ltd., College of Medicine, Pusan National University, 10 Amidong-1-Ga, Seogu, Pusan 602-739, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCT 02-JAN-2003
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Mobiluncus curtisii DNA for 16S-23S rRNA internal transcribed
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1 (bases 1 to 473)
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Mobiluncus mulieris 16S-23S ribosomal RNA intergenic spacer
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1. 458
/organism="uncultured bacterium ECS7"
/mol Lype="genomic DNA"
/db xref="taxon:122037"
/clone="ECS7"
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Yu, Z. and Mohn, W.W.

Sucerial diversity and community structure in an aerated lagoon revealed by ribosomal intergenic spacer analyses and 168 ribosomal DNA sequencing by ribosomal intergenic spacer analyses and 168 ribosomal DNA sequencing microbiol. 67 (4), 1565-1574 (2001)

L. Appl. Environ. Microbiol. 67 (4), 1565-1574 (2001)

E. 2178605

D. 11282606

S. Yu, Z. and Mohn, W.W.

Direct Submission

L. Submitted (26-UUL-2000) Microbiology and Immunology, University of British Columbia, #300-6174 University Blvd., Vancouver, BC V6T 123, Canada
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1. 497

/ Organiam="uncultured green non-sulfur bacterium Kmlps6-20"

/mol_type="genomic DNA"

/db xref="kaxon:135383"

/clone="kmlps6-20"

<1. -497

/product="16S ribosomal RNA"
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AF317470
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                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumbar, J., Barns, S.M., Ticknor, L.O. and Kuske, C.R.
Empirical and theoretical bacterial diversity in four Arizona soils
Appl. Environ. Microbiol. 68 (6), 3035-3045 (2002)
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Uncultured soil bacterium clone S13 16S ribosomal RNA gene, partial
                                                             Direct Submission
Submitted (14-OCT-1998) Shinya Sameshima, University of Tokyo,
Department of Biology; 3-8-1 Komaba, Meguro-ku, Tokyo 153-8902,
Japan (E-mail:897/216@hongo.ecc.u-tokyo.ac.jp, Tel:+81-3-5454-6652,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [Dunbar, J., Barns, S.M., Ticknor, L.O. and Kuske, C.R. Dunbar, J., Barns, S.M., Ticknor, L.O. and Kuske, C.R. Direct Submission

Submitted (26-ABR)

Laboratory, M888, Los Alamos, NM 87545, USA

Location/Qualifiers
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/isolation_source="pinyon-juniper forest soil"
/clone="813"
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/product="168 ribosomal RNA"
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/product="16S ribosomal RNA"
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                                                                                                                                                                                                                                                                        100.0%; Score 20; 100.0%; Pred. No.
                                                                                                                                                              /organism="endosymbiont
/mol_type="genomic DNA"
/db_xref="taxon:84570"
<1._.>570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uncultured soil bacterium
uncultured soil bacterium
Bacteria; environmental samples.
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   based on molecular evidences
Unpublished
2 (bases 1 to 570)
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                                                                                                                         Fax:+81-3-5454-4322)
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                                                  Sameshima, S.
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Best Local Similarity
Matches 20; Conserv
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                                 REFERENCE
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AUTHORS
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AF507717
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BCT 14-SEP-2003

linear

DNA

617 bp

AY369151

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/mol_type="genomic DNA"
/strain="Toro3A"
/strain="Toxo3A"
/bx zef="taxon:104629"
/noce="sequence derived from a single PCR amplicon
obtained from the gastric mucosa of a bull from Venezuela"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF31/470
Candidatus Helicobacter bovis strain Toro3A:16S ribosomal RNA gene, partial sequence.
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                    Bacteria; environmental samples.

1 (bases 1 to 617)

1 Sheng, X., Yang, H. and Li, D.
Analysis of the microbial community composition and transition in the activated sludge of a lab-scale deammonification reactor by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 827)
Gueneau, P., Fuenmayor, J., Aristimuno, O.C., Cedeno, S., Baez, E., Reyes, N., Michelangeli, F. and Dominguez-Bello, M.G.
Are goats naturally resistant to gastric Helicobacter infection?
Vet. Microbiol. 84 (1-2), 115-121 (2002)
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                                                                                                                                                                                                                                                                           Zheng,X., Yang,H. and Li,D.
Direct Submission
Submitted (18-AUG-2003) School of Life Science and Technology,
Shanghai Jiaotong University, No.800, Dongchuan Road, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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/organism="uncultured bacterium"
/mol_type="genomic DNA"
/db xref="t=xxxn:77133"
/clone="F-OTU12"
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100.0%; Pred. No. 40;
live 0; Mismatches 0;
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Submitted (27-OCT-2000) CBB, IVIC, Km 11
Pipe Miranda, Venezuela
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="16S ribosomal RNA"
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GI:34555665
                                          uncultured bacterium uncultured bacterium
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Gueneau de Novoa,P.
                                                                                                                                                                                                                                                         (bases 1 to 617)
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                                                                                                                                                                                                            molecular methods
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UBA309647 910 bp DNA linear BCT 06-JUN-2003
Uncultured Chloroflexaceae group bacterium 16S rRNA gene, clone
P6-C12.
                                           Nucbel, U.
Direct Submission
Direct Submission
Submitted (09-FBB-2001) Nucbel U., Molekulare Systematik und Submitted (09-FBB-2001) Nucbel U., Molekulare Systematik und Schotlogie, Deutsche Sammlung von Mikroorganismen und Zellkulturen, Mascheroder Weg 1B, Braunschweig, 38124, GERMANY
iocation/Qualifiers
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AJ309647.
AJ309647.1 GI:15552893
AJ309647.1 GI:15552893
Informal RNA, 168 rRNA gene.
uncultured Chloroflexales bacterium
uncultured Chloroflexales bacterium
Bacteria; Chloroflexi; Chloroflexales; environmental samples.
Information of the control of th
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/mol_type="genomic DNA"
/db_xref="taxon:152575"
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/gene="16S rRNA"
/product="16S ribosomal RNA"
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/gene="16S rRNA"
/product="16S ribosomal RNA"
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/db_xref="taxon:152575"
/clone="P6-C03"
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                             (bases 1 to 902)
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Best Local Similarity 100.
Matches 20; Conservative
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Direct Submission
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AUTHORS
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UBA309647
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AY220719
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Gallagher, J. M., Carton, M., Eardly, D. F. and Patching, J. W.
Erokaryotic community structure and biodiversity in deep waters of the NE Atlantic
Unpublished
2 (bases 1 to 857)
Gallagher, J. M., Carton, M., Eardly, D. F. and Patching, J. W.
Direct Submission
Submitted (17-JAM-2003) Microbiology, NUI, Galway, University Rd.,
Galway, Rep. of Ireland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="uncultured alpha proteobacterium"
/mol_type="genomic DNA"
/isolation source="water column, Porcupine Abyssal Plain,
Northeast Atlantic Ocean"
/db xref="tracon:91750"
/clone="WCPAPIS"
/environmental_sample
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AJ309645.
AJ309645.1 GT:15552891
IGS ribosomal RNA, 16S rRNA gene.
Uncultured Chloroflexales bacterium
SM uncultured Chloroflexies bacterium
Bacteria, Chloroflexi, Chloroflexales, environmental samples.
E 1 (asses 1 to 902)
Nubel, U., Bateson, M.M., Madigan, M.T., Kuhl, M. and Ward, D.M.
Diversity and distribution in hypersaline microbial mats of bacteria related to Chloroflexus spp
L Appl. Environ. Microbiol. 67 (9), 4365-4371 (2001)
                                                                                                                                         Gaps
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uncultured alpha proteobacterium
Bacteria; Proteobacteria; Alphaproteobacteria; environmental
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                              Length 827
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/product="16S ribosomal RNA"
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                                                                                    Score 20; DB
Pred. No. 37;
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Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches
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Length 936; 0; Indels

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Submitted (24-FBB-1998) Plant and Microbial Biology, University of California, Berkeley, 111 Koshland Hall, Berkeley, CA 94720, USA Location/Qualifiers
                                                    1. .936
/organism="uncultured eubacterium WCHA1-16"
/mol type="genomic DNA"
/db xref="ferials"="ferials" /clone="ferials" /clone="ferials" /clone" /note="isolated from a contaminated aquifer"
                                                                                                                                                          <1. .>936
/product="168 ribosomal RNA"
                                                                                                                                                                                                                          100.0%; Score 20; DB
100.0%; Pred. No. 35;
ive 0; Mismatches
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                                                                                                         UBA309611 911 bp DNA linear BCT 06-JUN-2003
Uncultured Chloroflexaceae group bacterium 16S FRNA gene, clone
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Uncultured eubacterium WCHA1-16 16S ribosomal RNA gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-FEB-2001) Nuebel U., Molekulare Systematik und Oekologie, Deutesche Sammlung von Mikroorganismen und Zellkulturen, Mascheroder Weg 1B, Braunschweig, 38124, GERMANY Location/Qualifiers
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AJ309611.1 GI:15552857
AJ309611.1 GI:15552857
Uncultured Chloroflexales bacterium
uncultured Chloroflexales bacterium
Bacteria, Chloroflexi, Chloroflexales; environmental samples.
I (bases I to 911)
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Appl. Environ. Microbiol. 67 (9), 4365-4371 (2001)
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uncultured eubacterium WCHA1-16
Bacteria; candidate division OP11; environmental samples.
1 (bases 1 to 936)
Dojka,M.A., Hugenholtz,P., Haack,S.K. and Pace,N.R.
Microbial diversity in a hydrocarbon- and
chlorinated-solvent-contaminated aquifer undergoing intri-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="uncultured Chloroflexales bacterium"
/mol_type="genomic DNA"
/dD_xref="taxon:152575"
/clone="p4-D01"
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Direct Submission
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98432811
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     GGAGGAAGGCGAGGATGACG 799
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/gene="16S rRNA"
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Uncultured bacterium partial 168 rRNA linear BCT 29-NOV-2002 AJ519648.

AJ519648.1 GI:26005694
168 ribosomal RNA; 168 rRNA gene.
uncultured bacterium
Bacteria. Aucultured bacterium
Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                 Geissler, A., Tzvetkova, T., Flemming, K. and Selenska-Pobell, S. Comparison of natural bacterial communities found in uranium mining waste piles and mill tailings Unpublished
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Selenska-Pobell,S.I.
Direct Submission
Submitted (28-NOV-2002) Selenska-Pobell S.I., Molecular
Microbiology, Institute of Radiochemistry, FZR, P.O.B. 51 01 19,
D-01314 Dresden, GERMANY
Location/Qualifiers
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Bakterielle Diversitaet in Erdproben aus Uranabfallhalden
Unpublished
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/mol type="rRNA"
/isolation_source="uranium mill tailings, soil fisolation_source="uranium mill tailings, soil follow_ref="taxon:77="uranium mill tailings, soil follow="sh768">-AG-uranium mill tailings, soil follow="sh768">-AG-uranium mill tailings, soil follow="sh7688-AG-14"
/clone="sh7688-AG-14"
/clone="ib="ds8-1404R"
/country="USA:Shiprock, New Mexico"
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/product="16S ribosomal RNA"
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Gaps

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Hongoh, Y., Ohkuma, M. and Kudu, ...
Direct Submission
Direct Submission
Direct Submission
Direct Submission
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Direct Submission
Submitted (26-701. 2002) Yuichi Hongoh, Japan Science and Technology
Corporation (357), Bio-Recycle Project, International Cooperative
Research Project; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:yhongo@postman.riken.go.jp, Tel:81-48-467-9546,
Fax:81-48-462-4672)
Fax:81-48-462-4672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF229791 1318 bp DNA linear BCT 01-FEB-2001
Uncultured bacterium TA18 16S ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1313
/organism="uncultured Bubacteriaceae bacterium"
/mol_type="genomic DNA"
/isolation_source="PCR-derived sequence from termite gut
homogenate"
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uncultured Bubacteriaceae bacterium
Bacteria; Firmicutes; Clostridia; Clostridiales; Bubacteriaceae;
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AB088955
AB088955.1 GI:27530167
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Molecular analysis of bacterial microbiota in the gut of the termite Reticulitermes speratus (Isoptera, Rhinotermitidae)
F.M. Microbiol. Ecol. 44, 231-242 (2003)
Hongoh,Y., Ohkuma,M. and Kudo,T.
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                                  100.0%; Score 20; DB 1; Length 1298; 100.0%; Pred. No. 32;
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(db_xref="taxon:203524"
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1 (bases 1 to 1318)

Mu,J.H., Liul, M.T., Tseng,I.C. and Cheng,S.S.
Characterization of microbial consortia in a
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/country="Japan:Saitama, Ogose"
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Mullins, T.D., Britschgi, T.B., Krest, R.L. and Giovannoni, S.J.
Genetic comparisons reveal the same unknown bacterial lineages in
Atlantic and Pacific Bacteriolahkton communities
Limnol. Oceanogr. 40 (1), 147-158 (1995)
Original source text: Alpha proteobacterium sp (clone: SAR102) DNA.
Location/Qualifiers
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Brofft, J.B., Shimkets, L.J. and McArthur, J.V.
Brofft, J.B., Shimkets, L.J. and McArthur, J.V.
Direct Submission
Submitted (24-UN-2002) Microbiology, University of Georgia, 527
Biological Sciences, Athens, GA 30602, USA
Location/Qualifiers
1. 1255
1. 1255
                                  AF524023 1255 bp DNA linear BCT 26-DEC-2
Uncultured bacterium clone FW128 16S ribosomal RNA gene, partial
                                                                                                                                                   uncultured bacterium
Bacteria; environmental samples.

[ bases 1 to 1255)
Brofft, J.B., McArthur, J.V. and Shimkets, L.J.
Recovery of novel bacterial diversity from a forested wetland impacted by reject coal and an environmental macrosis.

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Search completed: August Job time : 877,663 secs

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Candidatus Helicobacter bovis
Candidatus Helicobacter bovis
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacterae; Helicobacter.
1 (bases 1 to 1335)
De Groote, D., van Doorn, L. J., Ducatelle, R., Verschuuren, A.,
Tilmant, K., Quin, W. G., Haesebrouck, F. and Vandamme, P.
Phylogenetic characterization of Candidatus Helicobacter bovis', a new gastric helicobacter in cattle
1nt. J. Syst. Bacteriol. 49 Pt 4, 1707-1715 (1999)
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AF127027.1 GI:6018194
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                                                                                                                                     Submitted (01-FEB-2000) Department of Environmental Engineering, National Cheng Kung University, 1 University Road, Tainan 701, Taiwan, ROC
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terephthalate-degrading anaerobic granular sludge system
Microbiology 147 (Pt 2), 373-382 (2001)
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Wu,J.H., Liu,W.T., Tseng,I.C. and Cheng,S.S.
Direct Submission
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1103 GGAGGAAGGCGAGGATGACG 1122

1 GGAGGAAGGCGAGGATGACG 20

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ing table: OLIGG_NUC chape 60.0 , Gapext 60.0 size : 0 1 unmber of hits satisfying chosen parameters: 6 I number of hits satisfying chosen parameters: 6 Inumber of hits satisfying chosen parameters: 7 Inumber of hits satisfying chosen parameters: 7 Inumber of hits satisfying chosen parameters: 7 Inumber of hits satisfying chosen: 7 Inumber of hits satisfying chosen: 7 Inumber of hits satisfying chosen parameters: 7 Inumper of hits satisfying chosen parameters: 7 Inumper of hits satisfying chosen parameters: 7 Inumper of hits satisfying chosen parameters: 7 Inumber of hits satisfying chosen parameters: 7 Inumper of hits satisfying chosen parameters: 7
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	1 2	025 Sequenc	m	D11230 Marinomonas	M19442 L.pneumophi	M19451 T.micdader	D11247 Vibrio chol	M19449 T.micdadei	M98449 Clostridium	M19444 L.pneumophi	LOSIS4 Sequence or LOSS98 Clostridium	M24643 F.bozemanae	M24642 F. dumoffii	D11220 Alteromonas D11248 Vibrio chol	D11224 Aeromonas s	E05163 Sequence of	M34/13 I.Maceacher D28569 Sphingomona	D28572 Sphingomona	D28575 Sphingomona	Dilz46 Vibito chol D11233 Photobacter	D11219 Aeromonas h	U46521 Unidentifie	Ais/3834 Unculture AY373835 Unculture	D11256 Vibrio loge	AX575429 Sequence	AF228141 Marine se	AF228146 Marine se	I28355 Sequence 7	BD011645 DNA OL1GO	AF045815 Unculture AF045823 Unculture	AJ421167 Unculture	AJ405022 unculture	AF045827 Unculture	1 6	istonella	5			linear PAT 07-JAN-2003			,				g mycopiasma contamination	
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FEATURES

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LPNRRDA02 131 bp rRNA linear BCT 23-JUL-1993
L.pneumophila (strain Chicago-2) 16S rRNA, partial, segment 2 of 3.
M19442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (30-ABR-1992) Kumiko Kita-Tsukamoto, University of Tokyo,
Ocean Research Institute; 1-15-1 Minamidai, Nakano-ku, Tokyo 164,
Japan (E_mail:tukamoto@aix3.ori.u-tokyo.ac.jp, Tel:03-3376-1251,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales,
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Kita-Tsukamcko-K., Oyaizu,H., Nanba,K. and Simidu,U.
Phylogenetic relationships of marine bacteria, mainly members of
the family Vibrionaceae, determined on the basis of 16S rRNA
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Legionella pneumophila
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
                        /organism='Artificial Sequence'
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93152464
                                                                                                                                                                            100.0%; Score 20; DB 6; I
llarity 100.0%; Pred. No. 1.1e+05;
Conservative 0; Mismatches 0;
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Location/Qualifiers

    .47
    Organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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/strain="IAM12914"
/db_xref="taxon:28254"
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Kita-Tsukamoto, K.
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16S ribosomal RNA.
2 of 3
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PR 31-MAY-1989 US 359158
PI DAVID J LANE, YOTSNA SHAH, AMELIA BUHARIN, WILLIAM G WEISBURG PC C1202/68, C12N15/09, C12N15/09, C12N15/00, C22N15/00 CC Synthesized probe for hybridization
                                                                                                                                                                                                                                                                                                                                                            PAT 04-APR-2003
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synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 47)
Lane, D.J., Shah,J., Buharin,A. and Weisburg,W.G.
Universal eubacteria nucleic acid probe and method
Patent: JP 2002051799-A 9 19-FEB-2002,
Artificial Sequence
N JP 2002051799-A/9
                                                                                                                                           ch 100.0%; Score 20; DB 6; Length 23; 1 Similarity 100.0%; Pred. No. 1.6e+05; 20; Conservative 0; Mismatches
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/noTe="Primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_txref="taxon:32630"
/noce="primer"
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Sequence 1 from Patent WO03014382.
AX709025
                    location/Qualifiers
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 Minerva Biolabs GmbH (DE)
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JP 2002051799-A/9.
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artificial sequences.
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Tatlockia micdadai
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Tatlockia.
1 (bases 1 to 131)
Fox, K., Brown, A. and Schnitzer, G.
Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
                                                                                                                                                                                                                                                                                                                                                                                  Brown, A., Fox, K.F. and Schnitzer, G. Tatlockia, a genetically and chemically distinct group of bacteria: Proposal to transfer Legionella maceachernii (Brenner, et al.) to the genus Tatlockia as Tatlockia maceachernii comb. nov Syst. Appl. Microbiol. 14, 52-56 (1991) ooriginal source text: T.micdadei (ATCC 33346; strain Pgh-12) ribosomal RNA.
                                                           AMRRDB02 131 bp rRNA linear BCT 23-JUL-1993 micdadei (strain Pgh-12) 16S rRNA, partial, segment 2 of 3.
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Kita-Tsukamoto, K.

Biract Submission

Biract Submission

Submitted (30-APR-1992) Kumiko Kita-Tsukamoto, University of Tokyo, Ocean Research Institute; 1-15-1 Minamidai, Nakano-ku, Tokyo 164, Japan (B-mail:tukamoto@aix3.ori.u-tokyo.ac.jp, Tel:03-3376-1251, Fax:03-3375-6716)
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Kitza-Tsukamoto,K., Oyaizu,H., Nanba,K. and Simidu,U.
Phylogenetic relationships of marine bacteria, mainly members
the family Vibrionaceae, determined on the basis of 16S rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae
Vibrio cholerae
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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2 (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Tatlockia micdadei"
/mol_type="rRNA"
/db_xref="taxon:451"
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/organism="Vibrio cholerae"
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16S ribosomal RNA.
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                                      Fox, K., Brown, A. and Schnitzer, G.
Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
                                                                                                                                     Brown, A., Fox, K.F. and Schnitzer, G. Tatlockia, a genetically and chemically distinct group of bacteria: Proposal to transfer Legionella maceachernii (Brenner, et al.) to the genus Tatlockia as Tatlockia maceachernii comb. nov Syst. Appl. Microbiol. 14, 52-56 (1991)
Original source text: L.pneumophila (ATCC 33215; strain Chicago-2) ribosomal RNA.
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1 (Bases 1 to 131)

Fox K. Brown, A. and Schnitzer, G.
Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic implications
Syst. Appl. Microbiol. 11, 135-139 (1989)
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Original source text: Tamicadaei (strain PPA-JC) ribosomal RNA.
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Tatlockia micdadei
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
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100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                      /organism="Legionella pneumophila"
/mol_type="rRNA"
/db_xref="taxon:446"
                                                                                         Syst. Appl. Microbiol. 11, 135-139 (1989)
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About 250 bp after segment 1.
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/product="168 ribosomal RNA"
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T.micdadei (strain PPA-JC) 168 1
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/db_xref="taxon:451"
                                                                                                                                                                                                                                                                                Location/Qualifiers
Legionellaceae; Legionella
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M19451.1 GI:176096
16S ribosomal RNA.
1 of 3
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TAMRRD01
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LPNRRDC02
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E05154
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2 (sites)
2 (sites)
Brown, A., Pox, K.F. and Schnitzer, G.
Brown, A., a genetically and chemically distinct group of bacteria:
Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov
syst. Appl. Microbiol. 14, 52-56 (1991)
Original source text: T.micdadei (ATCC 33218; strain TATLOCK)
                                                                                                                                                                                                                                                               TAMRRDA02 133 bp rRNA linear BCT 23-JUL-1993
T.micdadei (strain TATLOCK) 16S rRNA, partial, segment 2 of 3.
M19449
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Clostridium sp. 165 ribosomal RNA (165 rRNA) gene, partial
sequence.
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Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
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Clostridium sp.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
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Galindo,I., Rangel-Aldao,R. and Ramirez,J.L.
A combined polymerase chain reaction-colour development
hybridization assay in a microtitre format for the detection of
                                                                                                                  Gaps
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Tatlockia micdadei
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Tatlockia.
1 (bases 1 to 133)
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                                                                           Query Match
100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 5.9e+04;
Conservative 0; Mismatches 0;
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/mol_type="rRNA"
/db_xref="taxon:451"
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About 250 bp after segment 1.
/mol_type="rRNA"
/strain="IID 935"
/db_xref="taxon:666"
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16S ribosomal RNA.
2 of 3
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16S ribosomal RNA.
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TAMRRDA02
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Brown, A., Fox, K.F. and Schnitzer, G.
Tatlockia, a genetically and chemically distinct group of bacteria:
Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov
Syst. Appl. Microbiol. 14, 52-56 (1991)
Original source text: L.pheumophila pneumophila (ATCC 33152; strain
'Philadelphia-i) ribosomal RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fox,K., Brown,A. and Schnitzer,G.
Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
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L pneumophila (strain Philadelphia-1) 16S rRNA, partial, segment 2
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Legionella pneumophila
Bacteria, Froteobacteria; Gammaproteobacteria, Legionellales;
Legionellaceae; Legionella.
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Clostridium spp
Appl. Microbiol. Biotechnol. 39 (4-5), 553-557 (1993)
93356986
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/mol_type="rRNA"
/db_xref="taxon:446"
<1. ->137
/product="16S ribosomal RNA"
About 250 bp after segment 1.
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100.0%; Pred. No. 5.8e+04;
iive 0; Mismatches 0;
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100.0%; Score 20; DB 1, I
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 20; Conservative 0; Mismatches 0;
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2 (sites)
                                                                                      Original source text: Clostridium sp. Maracabo) (library: EMBL4-LBB) DNA. Location/Qualifiers
                                                                                                                                                                                 /mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/db_xref="taxon:1506"
1. .137
                                                                                                                                                                                                                                                                                                   <1. .>137
/gene="16S rRNA"
/product="16S ribosomal RNA"
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                                                                                                                                                                                                                                                                             /gene="16S rRNA"
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M19444.1 GI:175178
16S ribosomal RNA.
2 of 3
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Best Local Similarity 100.
Matches 20; Conservative
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Fox, K., Brown, A. and Schnitzer, G.
Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
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2 (bases 1 to 140)

Brown, A., Fox, K.F. and Schnitzer, G.

Tatlockia, a genetically and chemically distinct group of bacteria:

Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov
syst. Appl. Microbiol. 14, 52-56 (1991)

Original source text: Fluoribacter bozemanae (strain MI-15) rRNA.
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Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
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                                                                                          Gaps
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Legionellaceae; Fluoribacter.
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Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales,
Legionellaceae, Fluoribacter.
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                                                      Score 20; DB 1; Length 138;
Pred. No. 5.8e+04;
Mismatches 0; Indels
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16S ribosomal RNA; ribosomal RNA small subunit.
2 of 3
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168 ribosomal RNA; ribosomal RNA small subunit.
2 of 3
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2 (bases 1 to 140)
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About 243 bp after segment 1.
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     ribosomal DNA gene"
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                                                                                                                              1 GCAAACAGGATTAGATACCC 20
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/strain="MI-15"
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                                                      Query Match
Best Local Similarity 100.0%; P. Matches 20; Conservative 0;
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Best Local Similarity
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LPNBMRRN02
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COMMENT
FEATURES
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TITLE
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AUTHORS
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E05154 117 bp DNA linear PAT 29-SEP-1997 Sequence of a DNA fraction prepared by a restriction enzyme HAP II Income DNA coding for E.coli 168 ribosome RNA.
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Location/Qualifiers
1 .138
/organism="Clostridium butyricum"
/mol_type="unassigned DNA"
/db_xref="taxon:1492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCT 28-MAR-1994
                                                 E05154
B05154.1 G1:2173347
UP 1993192147-A/26.
UP 1993192147-A/26.
UP 1993192147-A/26.
UP 1993192147-A/26.
UP 1993192147-A/26.
UP Scherichia coli
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriacea, Enteropacteriacea, Escherichia.

I (bases 1 to 137)
---- CEMIRNCE
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16S ribosomal DNA.
Clostridium butyricum
Clostridium butyricum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (gites)
Galindo,I., Rangel-Aldao,R. and Ramirez,J.L.
Galindo,I., Rangel-Aldao,R. and Ramirez,J.L.
A combined polymerase chain reaction-colour development
hybridization assay in a microtitre format for the detection of
Clostridium spp
Appl. Microbiol. Biotechnol. 39 (4-5), 553-557 (1993)
9336986

    1. 7138
/product="16S ribosomal RNA"
/note="corresponds to position 703 of the E. coli 16S

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Galindo-Castro, I.F., Rangel, R. and Ramirez, J.L.
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Clostridium butyricum 16S ribosomal DNA gene.
                                                                                                                                                                                                                METHOD FOR SPECIFYING DNA BASE SEQUENCE
Patent: JP 1993192147-A 26 03-AUG-1993;
KIRIN BIBARETSUJI KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                        15-NOV-1991 JP 1991300882
SHIRASU YOSHIHARU
C12N15/00,C12Q1/06,C12Q1/68;
strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                topology: Linear;
*source: strain=K12.
Location/Qualifiers
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                                                                                                                                                                                                                                                                       Escherichia coli
JP 1993192147-A/26
03-AUG-1993
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Unpublished (1993)
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CLORDNA16S
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TITLE
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ORIGIN

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AUTHORS Brown, A., Fox, K.F. and Schnitzer, G.

TITLE Tatlockia, a genetically and chemically distinct group of bacteria:
Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov

JOURNAL Syst. Appl. Microbiol. 14, 52-56 (1991)

COMMENT Tibosomal RNA.
FEATURES Location/Qualifiers

Source Acation/Qualifiers

1. 140

1. 140

1. 140

Anol. type="rRNA"

Anol. type="rR
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100.0%; Score 20; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 20; Conservative 0; Mismatches 0; Indels
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4, 2004, 07:44:15

Search completed: August Job time: 877,663 secs

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6747726 Total number of hits satisfying chosen parameters: 0 Word size :

3373863 segs, 2124099041 residues

Gapop_60.0 , Gapext 60.0

OLIGO_NUC

Scoring table:

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:* geneseqn2003cs:* geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2004s: 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abl59792 Neisseria Abl59802 Rhodospir Abl59802 Rhodospir Abl59793 Actinobac Abl59793 Actinobac Abl59793 Actinobac Abl59793 Actinobac Abr6512 Streptoco Acd97427 Human col Abr74330 Mycoplasm Apq20319 Region of Abr74330 Mycoplasm Aqq20319 Region of Add2946 Human col Acd92548 E. faeciu Acd92910 Human col Acd92910 Human col Acd92911 Human col Acd92918 Human col Acd92918 Human col Acd92918 Human col Acd92108 Human col	Aaz80671 Human col
ABL59792 ABL59791 ABL59802 ABL59802 ABL59800 ABL59800 ABN66212 ABV74330 AAQ20319 AAQ20319 ACD92986 ACD92089 ACD92089 ACD92089 ACD92108 AAQ0938	AAZ80671
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ALIGNMENTS

RESULT 1

Mollicutes sp; Mycoplasma; 16S rRNA; infection; PCR; primer; ss. Mycoplasma 16S rRNA gene PCR primer SEQ ID NO 2. ВР. 25-MAR-2002; 2002WO-DE001154. ABV74328 standard; DNA; 23 29-JAN-2003 (first entry) WO200277271-A2. Mycoplasma sp. 03-OCT-2002. ABV74328; ABV74328

25-MAR-2001; 2001DE-01015749. (MINE-) MINERVA BIOLABS GMBH.

Schramm C; Vollenbroich D,

WPI; 2003-040591/03.

Control plasmid, useful as internal standard in amplification method for detecting Mycoplasma, contains primers that recognize parts of the Mycoplasma 16S rRNA gene.

Claim 2; Page 15; 25pp; German.

The invention relates to a control plasmid (A) containing: (a) primers that recognize a segment of the 16S rRNA-encoding gene in the Mycoplasma genome, and (b) between the primers an amplicon that includes the sequence (i). (A) is used as a control in a PCR method for detecting Mycoplasma in biological materials, e.g. for diagnosing infections or control for PCR detection of cell cultures. (A) provides an internal method is more sensitive and specific than known processes, providing real-time PCR, has a broad dynamic and linear measurement range, allowing accurate quantitation. The present sequence is that of a Mycoplasma 16S rRNA gene PCR primer of the invention

Gaps

Sequence 24 BP; 9 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Sequence 23 BP; 9 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

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The present invention describes a method for identifying a microorganism by comparing a composite sequence (I) of a ribosomal RNA gene region with TRNA wegion sequences of unknown microorganisms in a database and identifying the region in the database that matches with (I). (I) is generated by simultaneously obtaining nucleotide base sequence data from very copy of the rRNA gene region in the genome of the unknown microorganism by generating (I) and entering it into a first data register of a programmable computer, comparing the first data register is with reference data registers that encode a unique composite rRNA sequence corresponding to (I) and correlated with unique microorganism sequence corresponding to (I) and correlated with unique microorganism species name, and displaying the unique microorganism name correlated with the best matching first data register. The method is useful for identifying microorganisms which are useful in a variety of fields including human medicine, veterinary medicine, agriculture, food science and industrial microbiology. The microorganisms found in patients of Microorganism identification is also useful for monitoring food safety by microorganism is also useful for monitoring food affety by microorganisms whence an also be identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial; 16S rRNA; identification; polymorphism; microorganism; classification; primer; human medicine; veterinary medicine; agriculture; food science; industrial microbiology; infectious disease; food safety;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an unknown microorganism by generating a composite sequence of its ribosomal RNA gene region and comparing with composite ribosomal RNA region sequences of distinct microorganisms in a database.
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0
DB 7; Length 23;
                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown bacterial 16S rRNA gene primer 0776F SEQ ID NO:9.
    100.0%; Score 20; DB 7
ilarity 100.0%; Pred. No. 0.1;
Conservative 0; Mismatches
                                                                                                                                                           1 GCAAACAGGATTAGATACCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA39031 standard; DNA; 24 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith DH, Dodge DE;
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                                        Similarity
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    Query Match
Best Local Simi
Matches 20;
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AAA39031
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This invention describes a novel device for detecting analytes in a sample. The device comprises a carrier surface which contains at least cone analytical region (including at least one immobilised binding partner for the analyte) and at least one immobilised binding partner for the analyte) and at least one immobilised binding partner for the analyte) and at least one sometimes of the amplification and detection of (i) bacterial species associated with pardontitis, (ii) gene expression patterns and (iii) single-nucleotide polymorphisms (SNP'S). The device provides reproducible, rapid and simple colymorphisms (SNP'S). The device provides reproducible, rapid and simple pardontities for the control step is required and system costs are not exactly the same series of operations as the analytical regions, so no extra time for the control step is required and system costs are not stored for archaving, the control results are also saved. Many different analytes can be detected simultaneously and controls for many different anelytes can be detected simultaneously and controls for many different anelytes can be detected simultaneously and controls for many different anoligonucleotide associated with the detection of 165 rRNA from various in the control is used to illustrate the device of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Device for determining analytes, useful e.g. for detecting bacteria that cause parodontitis, comprises a surface with immobilized analytical and
                                                                                                                                                                                                                                                                                                                                                                                          Probe, detection, primer; 16S rRNA, amplification; parodontitis, SNP, gene expression pattern; single-nucleotide polymorphism; ss.
                                         Gaps
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100.0%; Score 20; DB 3; Length 24; 100.0%; Pred. No. 0.1; o; Indels ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LAMB-) LAMBDA LABOR MOLEKULARBIOLOGISCHE.
                                                                                                                                                                                                                                                                                                                                                       16S rRNA forward PCR primer SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 26; 51pp; German.
                                                                                   1 GCAAACAGGATTAGATACCC 20
                                                                                                                 2 GCAACAGGATTAGATACCC 21
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                                                                                                                                                                                                                                 ABX94830 standard; DNA; 37 BP
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Best Local Similarity 100.
Matches 20; Conservative
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es 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inidentified.
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Gaps

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GCAAACAGGATTAGATACCC 20

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Nucleic acid probes - specific for RNA of Eubacteria, for use in clinical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection, microorganism, 16S rDNA, 16S rRNA, identification, gene, microbial encephalitis, viral encephalitis, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis 16S rDNA fragment #3
                                                                                                 Probe 1739 to the 16s rRNA of Eubacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 14-16; 58pp; English.
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                    (revised)
(revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Buharin A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-007226/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNSY ) UNIV SYDNEY.
                                                                                                                                              ribosomal RNA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200210444-A1.
                                                                                                                                                                                                                                                                                                            31-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                        31-MAY-1989;
                    27-AUG-2003
09-JAN-2003
14-MAR-1991
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                                                                                                                                                                                                                              WO9015157-A
                                                                                                                                                                                                                                                                        13-DEC-1990
                                                                                                                                                                                      Eubacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           Lane DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel device for detecting analytes in a sample. The device comprises a carrier surface which contains at least one analytical region (including at least one immobilised binding partner for the analyte) and at least one control region which controls of the quality of analyte) and the device is particularly used for nucleic acid amplification and detection of (i) bacterial species associated with parodontitis, (ii) gene expression patterns and (iii) single-nucleotide polymorphisms (SNP's). The device provides reproducible, rapid and simple analysis of nucleic acid sequences. The control system is subjected to exactly the same series of operations as the analytical regions, so no extra time for the control step is required and system costs are not significantly more than for analysis without a control. If the device is stored for archiving, the control results are also saved. Many different analytes can be detected simultaneously and controls for many different analytes an oligomucleotide associated with the detection of 165 rRNA from various bacterial samples, which is used to illustrate the device of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Device for determining analytes, useful e.g. for detecting bacteria that cause parodontitis, comprises a surface with immobilized analytical and control agents.
                                                                                                                                                                                                                                                                        Probe; detection; primer; 16S rRNA; amplification; parodontitis; SNP; gene expression pattern; single-nucleotide polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                            16S rRNA detection associated positive control oligonucleotide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zehethofer K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37 BP; 11 A; 8 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LAMB-) LAMBDA LABOR MOLEKULARBIOLOGISCHE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCAAACAGGATTAGATACCC 20
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GCAAACAGGATTAGATACCC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Page 37; 51pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ10118 standard; DNA; 47 BP.
                                                                                                    ABX94859 standard; DNA; 37 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2002; 2002WO-AT000239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001; 2001AT-00001247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ronacher B,
                                                                                                                                                                                        11-JUL-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                       Unidentified
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invention

AAQ10118;

RESULT 5 AAQ10118/0

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20-FEB-2003

ABX94859;

RESULT 4 ABX94859

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Gaps

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WPI; 2002-404428/43.

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The present invention describes a method for determining the total microbial content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (I) or its complement having a nucleotide sequence which is comprised by 16S rDNA or 16S rENA, substantially conserved amongst two or more species of microorganism. (I) can be used (I) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus or prevalence of a particular genus or species of microorganism; in a sample; and (3) as a probe of identify microorganism at the genus or species level, and as a trap for total microbial daraget material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (I) is applicable to a range of industries including the medical, agricultural and industrial industries with specific uses including enviroprotection, bioremediation, medical diagnosis, water quality control or food quality control. (I) provides an ability to detect bacteria from samples which industries indicated by viable culture count methods and enables rapid differentiation of bacteria from viral infections within the rapid of the provides and that would in all practicality remain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                limited time constraints sometimes experienced in life-threatening clinical situations. ABLS9702 to ABLS9821 represent 168 rDNA fragments, and ABLS9822 to ABLS9830 represent primers and probes, used in the exemplification of the present invention
                                                           Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 168 rDNA or 168 rRNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection, microorganism, 16S rDNA, 16S rRNA, identification, gene, microbial encephalitis, viral encephalitis, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nadkarni MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptostreptococcus micros 16S rDNA fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                      Example 12; Fig 1C; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAACAGGATTAGATACCC 35
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Best Local Similarity
Local Similarity
Local Similarity
Local Similarity
Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNSY ) UNIV SYDNEY
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                                                                                                                               microorganism
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ABL59817
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microbial content in a sample, comparising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microbial content in a sample, comparising amplifying a target nucleotide sequence which is comprised by 16S rDNA or nor complement having a nuclectide sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of microorganism. (1) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identify may particular microorganism or species level, and as a trap for identify microorganisms at the genus or species level, and as a trap for identify microorganisms at the genus or species level, and as a trap for identify microorganism and viral encephalitis. (1) is applicable to a range of industries including the medical, agricultural and user sense in microbial and viral encephalitis. (1) is applicable to a range of industries including enviroprotection, broamediation, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which undetected or under-estimated by viable culture count methods and enables rapid differentiation of bacteria from viral infections within the rapid differentiations. Ablisy02 to Ablisy821 represent les robne, used in the constraint of the constraints sometimes experienced in life-threatening constraints sometimes experienced in life-threatening constraints of the propes. used in the
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                                                           Polymucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rNNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                     present invention describes a method for determining the total
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis 16S rDNA fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the present invention
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                                                                                                                                                                              Example 12; Fig 1C; 101pp; English.
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia trachomatis
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                                                                                                                                      microorganism.
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The present invention describes a method for determining the total microbial content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (1) or its complement having a nucleotide sequence which is comprised by 168 rDNA or 168 rRNA, substantially conserved amongst two or more species of microorganism. (1) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a particular microorganism or prevalence of a particular genus or species of microorganism at the genus or species level, and as a trap for cortify microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (1) is applicable to a range of industries including the medical, agricultural distinguishing between microbial and viral encephalitis. (1) is applicable to a range of industries including the medical, agricultural addistinguishing between microbial and viral encephalitis. (1) is applicable to a range of industries including the medical, agricultural control. (1) provides an ability to detect bacteria from samples which includent constraints sometimes experienced in life-threatening rapid differentiation of bacteria from viral infections within the limited time constraints sometimes experienced in life-threatening and ABL59822 to ABL59820 to ABL59821 represent 16S rDNA fragments, and ABL59822 to ABL59821 represent invention
                                                          Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene; microbial encephalitis; viral encephalitis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50 BP; 15 A; 11 C; 16 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martin FE, Nadkarni MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusobacterium nucleatum 16S rDNA fragment #3.
                                                                                                                                                                    Example 12; Fig 1C; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNSY ) UNIV SYDNEY.
                    WPI; 2002-404428/43.
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                                                                                                                                microorganism
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Matches
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The present introduction describes a meriou for determining the cotain content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microbraganisms. Also describes is an isolated polynucleotide (I) or its complement having a nucleotide sequence which is comprised by 168 rDNA or 168 rENA, substantially conserved amongst two or more species of microbraganism. (I) can be used: (I) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for dentifying a microbraganism, in a sample; (I) as a primer or probe for contentifying a microbraganism, in a sample. (I) can also be used to identifying a particular microorganism or species level, and as a trap for total microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (I) is applicable to a range of industries including the medical, agricultural and industries with specific uses including enviroprotection, bioremediation, medical diagnosis, water quality control or food quality control. (I) provides an ability to detect bacteria from samples which are difficult to cultivate and that would in all practicality remain cundetected or under-estimate and that would in all practicality remain cundetected or under-estimate and that would in all practicality remain cultimical situations. ABLS9702 to ABLS921 represent 165 rDNA fragments, and ABLS9822 to ABLS9810 represent primers and probes, used in the
                                                        Polynuclectide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                         present invention describes a method for determining the total
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exemplification of the present invention
                                                                                                                                                                   Example 12; Fig 1C; 101pp; English.
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Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
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                  WPI; 2002-404428/43.
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                                                                                                                               microorganism.
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ABL59786
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microbial content in describes a menical to versiminary die occidentation describes is an isolated amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (1) or its complement having a nucleotide sequence which is comprised by 16S rDNA or isolated polynucleotide (1) or its complement having a nucleotide sequence which is comprised by 16S rDNA or isolated polynucleotide (1) or its complement having a nucleotide sequence which is comprised by 16S rDNA or microorganism. (1) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus or prevalence of a particular genus or species level, and as a trap for identify microbial-derived target material; in assessing encephalitis and istinguishing between microbial and viral encephalitis. (1) is applicable to a range of industries including enviroprotection, bloremediation, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which bloremediation, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which indetected or under-estimated by viable culture count methods and enables capital situations. ABLS9902 to ABLS981 represent les robn fragments, used in the available of the constraints sometimes experienced in life-threatening constraints.
                                                           Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
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                                                                                                                                                                                                                 The present invention describes a method for determining the total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention
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                                                                                                                                                                    Example 12; Fig 1C; 101pp; English.
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                    WPI; 2002-404428/43.
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Best Local Similarity
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                                                                                                                             microorganism.
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the present invariances a mercina into determining the Cotal accordent in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (1) or its complement having a nucleotide sequence which is comprised by 16s rDNA or 16s FRNA, substantially conserved amongst two or more species of microorganism. (1) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for identifying a microorganism by its genus in a sample; and (3) as a primer or probe for identifying a microorganism by its genus in a sample; and (3) as a primer or probe for controlitying a microorganism by its genus in a sample; and (3) as a primer or probe for identifying a microorganism, in a sample; (1) can also be used to identify microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (1) is and industrial industries including the medical, agricultural and industrial industries with specific uses including enviroprotection, controlition, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which are difficult to cultivate and that would in all practicality remain undetected or under-estimated by viable culture count methods and enables control situations. ABLS9902 to ABLS9821 represent les rons within the constraints sometimes experienced in life-threatening constraints sometimes experienced in life-threatening constraints constraints and propes, used in the
                                                         Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rNNA, substantially conserved amongst two or more species of
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                                                                                                                                                                                                                 present invention describes a method for determining the total
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                                                                                                                                                                   Example 12; Fig 1C; 101pp; English.
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Best Local Similarity
                  WPI; 2002-404428/43.
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                                                                                                                            microorganism.
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Nadkarni MA;

Martin FE,

Hunter N, Jacques NA,

(UNSY) UNIV SYDNEY.

28-JUL-2000;

WPI; 2002-404428/43.

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The present invention describes a method for determining the total microbial content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst. 2 or more species of microorganisms. Also describes is an isolated polynucleotide (I) or its complement having a nucleotide sequence which is comprised by 16S rDNA or 16S FRAM, substantially conserved amongst two or more species of microorganism. (I) can be used: (I) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for identifying a microorganism by its genus in a sample, and (3) as a probe for identifying a particular microorganism or prevalence of a particular genus or species of microorganism or prevalence of a particular genus or species of microorganism or the genus or species level, and as a trap for total microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (I) is applicable to a range of industries including the medical, (I) is applicable to a range of industries including the medical, on as a trap for control. (I) provides an ability to detect bacteria from samples which secific uses including enviroprotection, bioremediation, medical diagnosis, water quality control or food quality control. (I) provides an ability to detect bacteria from samples which englid differentiation of bacteria from viral infections within the undetected or under-estimated by viable culture count methods and enables rapid differentiation of bacteria from viral infections within the culture count methods and enables reported in the count methods and enables or particular count methods and enables or partic
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                                                                     Polymucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
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                                                                                                                                                                                                    Example 12; Fig 1C; 101pp; English
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les 20; Conservative
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                        WPI; 2002-404428/43.
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                                                                                                                                                     microorganism
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Matches
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The present invention describes a method for determining the obtainment of the present invention describes a method for described amongst 2 or more species of sequence which is substantially conserved amongst 2 or more species of microcyanisms. Also describes is an isolated polynucleotide (1) or its complement having a nucleotide sequence which is comprised by 165 rDNA or 165 rRNA, substantially conserved amongst two or more species of incroorganism. (1) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for dentifying a microorganism by its genus in a sample; and (3) as a probe for identifying a particular microorganism or prevalence of a particular of genus or species of microorganism; in a sample; and (3) as a probe for identify microorganisms at the genus or species level, and as a trap for otal microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (1) is control. (1) provides an ability to detect bacteria from samples which control. (1) provides an ability to detect bacteria from samples which control. (1) provides an ability to detect bacteria from samples which control timeted time constraints sometimes experienced in life-threatening control. Or food quality control or indetected or undetected by viable culture count methods and enables rapid differentiation of bacteria from viral infections within the control or sublications ABLS9822 to A
                                                             Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection, microorganism, 16S rDNA, 16S rRNA, identification, gene, microbial encephalitis, viral encephalitis, ds.
                                                                                                                                                                                                                                    The present invention describes a method for determining the total
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50 BP; 14 A; 12 C; 17 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nadkarni MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Legionella pneumophila 16S rDNA fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Prec. ...
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                                                                                                                                                                                        Example 12; Fig 1C; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCAAACAGGATTAGATACCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 gcaaacaggarragaraccc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL59799 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-2001; 2001WO-AU000933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000AU-00009090.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Legionella pneumophila
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                                                                                                                                               microorganism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL59799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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Gaps

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Martin FE, Nadkarni MA;

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us-09-940-860-1.oligo.rng

WPI; 2002-404428/43

The present in a sample, comparising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microbial content in a sample, conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (I) or its complement having a nucleotide sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of microorganism. (I) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for determining the total microorganism by its genus in a sample; and (3) as a primer or probe for dentifying a particular microorganism or prevalence of a particular genus or species level, and as a trap for identify microorganisms at the genus or species level, and as a trap for total microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (I) is applicable to a range of industries including the medical, agricultural and industrial industries with specific uses including enviroprotection, bloremediation, medical diagnosis, water quality control or food quality control. (I) provides an ability to detect bacteria from samples which undetected or under-estimated by viable culture count methods and enables immited time constraints sometimes experienced in life-threatening climited situations. ABL59902 to ABL59821 represent les rbnA fragments, as a primer of the experience of in the comparation of the present incomparion or propersent primers and probes, used in the Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of present invention describes a method for determining the total Example 12; Fig 1C; 101pp; English.

Sequence 50 BP; 15 A; 11 C; 16 G; 8 T; 0 U; 0 Other;

exemplification of the present invention

100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; ive 0; Mismatches 0; Indels GCAAACAGGATTAGATACCC 35 1 GCAAACAGGATTAGATACCC 20 20; Conservative Query Match Best Local Similarity Matches g ð

ABL59801 standard; DNA; 50 BP. RESULT 15 ABL59801

ABL59801;

Caulobacter vibrioides 16S rDNA fragment #3.

(first entry)

18-JUL-2002

Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene; microbial encephalitis; viral encephalitis; ds.

Caulobacter vibrioides

WO200210444-A1

07-FEB-2002.

27-JUL-2001; 2001WO-AU000933.

28-JUL-2000; 2000AU-00009090.

(UNSY) UNIV SYDNEY

Martin FE, Nadkarni MA; Hunter N, Jacques NA,

Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rNNA, substantially conserved amongst two or more species of nicroorganism.

Example 12; Fig 1C; 101pp; English.

microbial content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (I) or its complement having a nucleotide sequence which is comprised by 165 rDNA or 165 rRNA, substantially conserved amongst two or more species of microorganism. (I) can be used: (I) as a primer or probe for determining the total microbial content in a sample, (2) as a primer or probe for dentifying a microorganism by its genus in a sample, and (3) as a probe for identifying a microorganism, in a sample, (I) can also be used to identify microorganism at the genus or species level, and as a trap for total microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (I) is and industrial industries including the medical, agricultural and industrial industries with specific uses including enviroprotection, bloremediation, medical disagnosis, water quality control or food quality control. (I) provides an ability to detect bacteria from samples which are difficult to cultivate and that would in all practicality remain entity of the same and enables and enables and enables time constraints sometimes experienced in life-threatening l situations. ABL59702 to ABL59821 represent 16S rDNA fragments, 9822 to ABL59830 represent primers and probes, used in the invention describes a method for determining the total rapid differentiation of bacteria from viral infections within the exemplification of the present invention The present clinical imited

Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;

. 0 100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; tive 0; Mismatches 0; Indels Conservative Similarity 20; Query Match Local Matches

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Gaps

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